



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 169177**

**TO: Jeffrey Parkin**  
**Location: rem/3D39/3C18**  
**Art Unit: 1648**  
**Friday, October 28, 2005**  
**Case Serial Number: 09/826115**

**From: Toby Port**  
**Location: Biotech-Chem Library**  
**REM-1A59**  
**Phone: 571-272-2523**  
  
**toby.port@uspto.gov**

### **Search Notes**

**Examiner Parkin,**

**See attached results.**

**If you have any questions about this search feel free to contact me at any time.**

**Thank you for using STIC search services!**

**Toby Port**  
**X22523**

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STIC-Biotech/ChemLib

169 170

mej

From: Parkin, Jeffrey  
Sent: Thursday, October 20, 2005 1:52 PM  
To: STIC-Biotech/ChemLib  
Subject: U.S. Serial No. 09/826,115 Sequence Search

Please search **SEQ ID NO.: 14** from U.S. Application No. **09/826,115** v. all relevant databases. Place results on **BOTH** paper and electronic format (i.e., disk, e-mail, etc.).

Thanks!

JSP  
REM 3D39  
2-0908

6/2/06

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OCT 20 2005  
STIC/BIOTECH DIV.  
(STIC)

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 01:14:34 ; Search time 164 Seconds  
(without alignments)  
56.599 Million cell updates/sec

Title: US-09-826-115a-14  
Perfect score: 118  
Sequence: 1 MGKRSAGSIMVLASLAVVIACAGA 24

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980a:\*
- 2: geneseqp1990a:\*
- 3: geneseqp2000a:\*
- 4: geneseqp2001a:\*
- 5: geneseqp2002a:\*
- 6: geneseqp2003a:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004a:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	100.0	24	6	Abp57858 West Nile
2	118	100.0	33	6	Abp57869 Signal se
3	118	100.0	685	6	Abp57874 Plaamid p
4	118	100.0	685	6	Abp57876 Plaamid p
5	118	100.0	685	6	Abp57875 Plaamid p
6	118	100.0	692	6	Abp57859 Plaamid p
7	96	81.4	24	6	Abp57864 St. Louis
8	96	81.4	681	6	Abp57863 Plaamid p
9	96	81.4	681	6	Abp57861 Plaamid p
10	96	81.4	692	6	Abp57862 Plaamid p
11	91	77.1	39	6	Abp57879 Signal se
12	91	77.1	697	6	Abp57860 Plaamid p
13	91	77.1	697	6	Abp57857 Plaamid p
14	89	75.4	23	8	Adm97134 Japanese
15	89	75.4	30	6	Abp57867 Signal se
16	89	75.4	1664	1	Abp80264 Sequence
17	89	75.4	3432	3	Abp807037 Japanese
18	78	66.1	32	4	Abp84905 Peptide f
19	78	66.1	970	1	Abp93305 Antigenic
20	78	66.1	970	2	Aar85479 Japanese
21	78	66.1	1295	2	Aar05597 Sequence
22	78	66.1	1295	2	Aar10424 Recombina
23	75	63.6	24	6	Abp57866 Signal se
24	52	44.1	808	5	Aac21528 Arabidops
25	52	44.1	808	8	Adn72641 Thale cre

## ALIGNMENTS

### RESULT 1

ABP57858  
ID ABP57858 standard; peptide; 24 AA.  
XX  
AC ABP57858;  
XX  
DT 07-FEB-2003 (first entry)  
XX  
DE West Nile virus JE signal peptide.  
XX  
KW Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;  
KW West Nile virus; JE signal.  
XX  
OS West Nile virus.  
XX  
FN WO200281754-A1.  
XX  
PD 17-OCT-2002.  
XX  
PF 04-APR-2002; 2002WO-US010764.  
XX  
PR 04-APR-2001; 2001US-00826115.  
XX  
(USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Chang GJ;  
WPI; 2003-058572/05.  
Novel isolated nucleic acid useful as vaccine for preventing flavivirus infection, comprises transcriptional unit encoding signal sequence of one flavivirus and immunogenic flavivirus antigen of a second flavivirus.  
Example 9; Page 120; 174pp; English.  
The invention relates to a novel nucleic acid comprising a transcriptional unit encoding a signal sequence of a structural protein of a first flavivirus and an immunogenic flavivirus antigen of a second flavivirus, where the transcriptional unit directs the synthesis of the antigen. The polynucleotide of the invention has virucide activity, and acts as a vaccine. A composition of the invention is useful for immunising a subject against infection by a flavivirus. The polynucleotide is useful as a vaccine for preventing flavivirus infection. The sequence represents the West Nile virus prM and E protein  
Sequence 24 AA;

26	51	43.2	79	4	AAG91144	C glutami
27	51	43.2	168	6	ABU23514	Protein e
28	51	43.2	412	4	AAG92132	C glutami
29	51	43.2	1377	5	ABP65418	Bifidobac
30	50	42.4	166	4	ABG17841	Novel hum
31	50	42.4	190	4	ABG17839	Novel hum
32	50	42.4	328	4	AAG90131	C glutami
33	50	42.4	385	4	AAG98923	E. coli g
34	50	42.4	426	4	ABG17840	Novel hum
35	50	42.4	443	6	ADA35782	Acinetoba
36	49.5	41.9	142	6	ABR40595	Oryza sat
37	49.5	41.9	424	6	ABR40859	Oryza sat
38	49	41.5	120	4	AAU86649	Novel hum
39	49	41.5	120	7	ABD59983	Connectiv
40	49	41.5	204	8	ADJ98193	Rickettsi
41	49	41.5	204	8	ADJ98191	Rickettsi
42	49	41.5	328	8	ADI24533	Human mod
43	49	41.5	648	5	AAU74395	Fructosyl
44	49	41.5	648	8	ADJ49485	Oil-assoc
45	48	40.7	405	8	ADN26045	Bacterial

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Query Match      100.0%; Score 118; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. NO. 9.4e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRSAGSIMWLASLAVVIACAGA 24
DB 1 MGRSAGSIMWLASLAVVIACAGA 24

RESULT 2
ABP57869
ID ABP57869 standard; peptide; 33 AA.
XX AC
XX ABP57869;
XX DT
XX 07-FEB-2003 (first entry)
XX DE
XX Signal sequence preceding prM protein in plasmid pCBWN.
XX KW
XX Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;
XX signal sequence.
XX OS
XX Unidentified.
XX PN
XX WO200281754-A1.
XX PD
XX 17-OCT-2002.
XX PF
XX 04-APR-2002; 2002WO-US010764.
XX PR
XX 04-APR-2001; 2001US-00926115.
XX PA
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI
XX Chang GJ;
XX DR
XX WPI; 2003-058572/05.
XX N-PSDB; ABV77547.
XX PT
XX Novel isolated nucleic acid useful as vaccine for preventing flavivirus
XX infection, comprises transcriptional unit encoding signal sequence of one
XX flavivirus and immunogenic flavivirus antigen of a second flavivirus.
XX Disclosure; Page 87; 174pp; English.
XX CC
XX The invention relates to a novel nucleic acid comprising a
XX transcriptional unit encoding a signal sequence of a structural protein
XX of a first flavivirus and an immunogenic flavivirus antigen of a second
XX flavivirus, where the transcriptional unit directs the synthesis of the
XX antigen. The polynucleotide of the invention has virucide activity, and
XX acts as a vaccine. A composition of the invention is useful for
XX immunising a subject against infection by a flavivirus. The
XX polynucleotide is useful as a vaccine for preventing flavivirus
XX infection. The sequence represents the signal sequence preceding the prM
XX protein in the plasmid pCBWN of the invention
XX Sequence 33 AA;

Query Match      100.0%; Score 118; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. NO. 1.3e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRSAGSIMWLASLAVVIACAGA 24
DB 1 MGRSAGSIMWLASLAVVIACAGA 24

RESULT 3
ABP57874
ID ABP57874 standard; protein; 685 AA.
XX AC
XX ABP57874;
XX DT
XX 07-FEB-2003 (first entry)

```

```

XX DE
XX Plasmid pCBD2-14-6 containing dengue-2 virus prM and E.
XX KW
XX Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;
XX pCBD2-14-6; dengue virus; DEN-2.
XX OS
XX Unidentified.
XX OS
XX Dengue-2 virus.
XX OS
XX Chimeric.
XX PN
XX WO200281754-A1.
XX PD
XX 17-OCT-2002.
XX PF
XX 04-APR-2002; 2002WO-US010764.
XX PR
XX 04-APR-2001; 2001US-00826115.
XX PA
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI
XX Chang GJ;
XX DR
XX WPI; 2003-058572/05.
XX N-PSDB; ABV77547.
XX PT
XX Novel isolated nucleic acid useful as vaccine for preventing flavivirus
XX infection, comprises transcriptional unit encoding signal sequence of one
XX flavivirus and immunogenic flavivirus antigen of a second flavivirus.
XX Example 20; Page 157-158; 174pp; English.
XX CC
XX The invention relates to a novel nucleic acid comprising a
XX transcriptional unit encoding a signal sequence of a structural protein
XX of a first flavivirus and an immunogenic flavivirus antigen of a second
XX flavivirus, where the transcriptional unit directs the synthesis of the
XX antigen. The polynucleotide of the invention has virucide activity, and
XX acts as a vaccine. A composition of the invention is useful for
XX immunising a subject against infection by a flavivirus. The
XX polynucleotide is useful as a vaccine for preventing flavivirus
XX infection. The sequence represents plasmid pCBD2-14-6, which contains
XX dengue-2 virus (DEN-2) prM and E proteins
XX Sequence 685 AA;

Query Match      100.0%; Score 118; DB 6; Length 685;
Best Local Similarity 100.0%; Pred. NO. 3.2e-09;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRSAGSIMWLASLAVVIACAGA 24
DB 1 MGRSAGSIMWLASLAVVIACAGA 24

RESULT 4
ABP57876
ID ABP57876 standard; protein; 685 AA.
XX AC
XX ABP57876;
XX DT
XX 07-FEB-2003 (first entry)
XX DE
XX Plasmid pCB8D2-2J-2-9-1 protein product.
XX KW
XX Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;
XX pCB8D2-2J-2-9-1; Japanese encephalitis virus; dengue-2 virus; DEN-2.
XX OS
XX Unidentified.
XX OS
XX Synthetic.
XX PN
XX WO200281754-A1.
XX PD
XX 17-OCT-2002.
XX

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PF 04-APR-2002; 2002WO-US010764.  
 XX  
 PR 04-APR-2001; 2001US-00826115.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Chang GJ;  
 XX  
 DR WPI; 2003-058572/05.  
 DR N-PSDB; ABV77549.  
 XX  
 XX Novel isolated nucleic acid useful as vaccine for preventing flavivirus  
 PT infection, comprises transcriptional unit encoding signal sequence of one  
 PT flavivirus and immunogenic flavivirus antigen of a second flavivirus.  
 XX  
 PS Example 20; Page 168-169; 174pp; English.  
 XX  
 CC The invention relates to a novel nucleic acid comprising a  
 CC transcriptional unit encoding a signal sequence of a structural protein  
 CC of a first flavivirus and an immunogenic flavivirus antigen of a second  
 CC flavivirus, where the transcriptional unit directs the synthesis of the  
 CC antigen. The polynucleotide of the invention has virucide activity, and  
 CC acts as a vaccine. A composition of the invention is useful for  
 CC immunising a subject against infection by a flavivirus. The  
 CC polynucleotide is useful as a vaccine for preventing flavivirus  
 CC infection. The sequence represents plasmid pCB9D2-2J-2-9-1, which  
 CC contains dengue-2 virus (DEN-2) prM, M and E, and Japanese encephalitis  
 CC virus E proteins  
 XX  
 SQ Sequence 685 AA;  
 Query Match 100.0%; Score 118; DB 6; Length 685;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-09;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGKRSAGSIMMLASLAVVIACAGA 24  
 Db 1 MGKRSAGSIMMLASLAVVIACAGA 24  
 |||||  
 RESULT 5  
 ABP57875  
 ID ABP57875 standard; protein; 685 AA.  
 XX  
 AC ABP57875;  
 XX  
 DT 07-FEB-2003 (first entry)  
 XX  
 DE Plasmid pCB9D2-IJ-4-3 protein product.  
 XX  
 KW Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;  
 KW pCB9D2-IJ-4-3; Japanese encephalitis virus; dengue-2 virus; DEN-2.  
 XX  
 OS Unidentified.  
 OS Synthetic.  
 XX  
 PN WO200281754-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 04-APR-2002; 2002WO-US010764.  
 XX  
 PR 04-APR-2001; 2001US-00826115.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Chang GJ;  
 XX  
 DR WPI; 2003-058572/05.  
 DR N-PSDB; ABV77548.  
 XX  
 XX Novel isolated nucleic acid useful as vaccine for preventing flavivirus  
 PT infection, comprises transcriptional unit encoding signal sequence of one

PT flavivirus and immunogenic flavivirus antigen of a second flavivirus.  
 XX  
 PS Example 20; Page 162-164; 174pp; English.  
 XX  
 CC The invention relates to a novel nucleic acid comprising a  
 CC transcriptional unit encoding a signal sequence of a structural protein  
 CC of a first flavivirus and an immunogenic flavivirus antigen of a second  
 CC flavivirus, where the transcriptional unit directs the synthesis of the  
 CC antigen. The polynucleotide of the invention has virucide activity, and  
 CC acts as a vaccine. A composition of the invention is useful for  
 CC immunising a subject against infection by a flavivirus. The  
 CC polynucleotide is useful as a vaccine for preventing flavivirus  
 CC infection. The sequence represents plasmid pCB9D2-IJ-4-3, which contains  
 CC dengue-2 virus (DEN-2) prM, M and E, and Japanese encephalitis virus E  
 CC proteins  
 XX  
 SQ Sequence 685 AA;  
 Query Match 100.0%; Score 118; DB 6; Length 685;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-09;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGKRSAGSIMMLASLAVVIACAGA 24  
 Db 1 MGKRSAGSIMMLASLAVVIACAGA 24  
 |||||  
 RESULT 6  
 ABP57859  
 ID ABP57859 standard; protein; 692 AA.  
 XX  
 AC ABP57859;  
 XX  
 DT 07-FEB-2003 (first entry)  
 XX  
 DE Plasmid pCBWN containing West Nile virus prM and E.  
 XX  
 KW Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;  
 KW pCBWN; West Nile virus.  
 XX  
 OS Unidentified.  
 OS West Nile virus.  
 OS Chimeric.  
 XX  
 PN WO200281754-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 04-APR-2002; 2002WO-US010764.  
 XX  
 PR 04-APR-2001; 2001US-00826115.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Chang GJ;  
 XX  
 DR WPI; 2003-058572/05.  
 DR N-PSDB; ABV77536.  
 XX  
 XX Novel isolated nucleic acid useful as vaccine for preventing flavivirus  
 PT infection, comprises transcriptional unit encoding signal sequence of one  
 PT flavivirus and immunogenic flavivirus antigen of a second flavivirus.  
 XX  
 PS Example 9; Page 124-125; 174pp; English.  
 XX  
 CC The invention relates to a novel nucleic acid comprising a  
 CC transcriptional unit encoding a signal sequence of a structural protein  
 CC of a first flavivirus and an immunogenic flavivirus antigen of a second  
 CC flavivirus, where the transcriptional unit directs the synthesis of the  
 CC antigen. The polynucleotide of the invention has virucide activity, and  
 CC acts as a vaccine. A composition of the invention is useful for  
 CC immunising a subject against infection by a flavivirus. The  
 CC polynucleotide is useful as a vaccine for preventing flavivirus

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CC infection. The sequence represents plasmid pCBWV, which contains West
CC nile virus prM and E proteins
XX
SQ Sequence 692 AA;

Query Match      100.0%; Score 118; DB 6; Length 692;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGKRSAGSIMWLASLAVVIACAGA 24
   |||||
Db 1 MGKRSAGSIMWLASLAVVIACAGA 24

RESULT 7
ABP57864
ID ABP57864 standard; peptide; 24 AA.
XX
AC ABP57864;
XX
DT 07-FEB-2003 (first entry)
XX
DE St. Louis encephalitis virus JE signal peptide.
XX
KW Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;
KW St. Louis encephalitis virus; JE signal.
XX
OS St. Louis encephalitis virus.
XX
PN WO200281754-A1.
XX
PD 17-OCT-2002.
XX
PF 04-APR-2002; 2002WO-US010764.
XX
PR 04-APR-2001; 2001US-00826115.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Chang GU;
XX
DR WPI; 2003-058572/05.
XX
N-PSDB; ABV77540.
XX
PT Novel isolated nucleic acid useful as vaccine for preventing flavivirus
PT infection, comprises transcriptional unit encoding signal sequence of one
PT flavivirus and immunogenic flavivirus antigen of a second flavivirus.
XX
PS Example 13; Page 149; 174pp; English.
XX
CC The invention relates to a novel nucleic acid comprising a
CC transcriptional unit encoding a signal sequence of a structural protein
CC of a first flavivirus and an immunogenic flavivirus antigen of a second
CC flavivirus, where the transcriptional unit directs the synthesis of the
CC antigen. The polynucleotide of the invention has virucide activity, and
CC acts as a vaccine. A composition of the invention is useful for
CC immunising a subject against infection by a flavivirus. The
CC polynucleotide is useful as a vaccine for preventing flavivirus
CC infection. The sequence represents the St. Louis encephalitis virus prM
CC and E protein JE signal sequence
XX
SQ Sequence 24 AA;

Query Match      81.4%; Score 96; DB 6; Length 24;
Best Local Similarity 87.5%; Pred. No. 2.1e-07;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGKRSAGSIMWLASLAVVIACAGA 24
   |||||
Db 1 MGKRSAGSIMWLASLAVVIAGTSA 24

RESULT 8
ABP57863

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ID ABP57863 standard; protein; 681 AA.
XX
AC ABP57863;
XX
DT 07-FEB-2003 (first entry)
XX
DE Plasmid pCBYF containing yellow fever virus prM and E.
XX
KW Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;
KW pCBYF; Yellow fever virus.
XX
OS Unidentified.
OS Yellow fever virus.
OS Chimeric.
XX
PN WO200281754-A1.
XX
PD 17-OCT-2002.
XX
PF 04-APR-2002; 2002WO-US010764.
XX
PR 04-APR-2001; 2001US-00826115.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Chang GU;
XX
DR WPI; 2003-058572/05.
XX
N-PSDB; ABV77540.
XX
PT Novel isolated nucleic acid useful as vaccine for preventing flavivirus
PT infection, comprises transcriptional unit encoding signal sequence of one
PT flavivirus and immunogenic flavivirus antigen of a second flavivirus.
XX
PS Example 14; Page 147-148; 174pp; English.
XX
CC The invention relates to a novel nucleic acid comprising a
CC transcriptional unit encoding a signal sequence of a structural protein
CC of a first flavivirus and an immunogenic flavivirus antigen of a second
CC flavivirus, where the transcriptional unit directs the synthesis of the
CC antigen. The polynucleotide of the invention has virucide activity, and
CC acts as a vaccine. A composition of the invention is useful for
CC immunising a subject against infection by a flavivirus. The
CC polynucleotide is useful as a vaccine for preventing flavivirus
CC infection. The sequence represents plasmid pCBYF, which contains yellow
CC fever virus prM and E proteins
XX
SQ Sequence 681 AA;

Query Match      81.4%; Score 96; DB 6; Length 681;
Best Local Similarity 87.5%; Pred. No. 7.3e-06;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGKRSAGSIMWLASLAVVIACAGA 24
   |||||
Db 1 MGKRSAGSIMWLASLAVVIAGTSA 24

RESULT 9
ABP57861
ID ABP57861 standard; protein; 681 AA.
XX
AC ABP57861;
XX
DT 07-FEB-2003 (first entry)
XX
DE Plasmid pCBPOW containing Powassan virus prM and E.
XX
KW Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;
KW pCBPOW; Powassan virus.
XX
OS Unidentified.
OS Powassan virus.

```



OS Chimeric.  
 XX WO200281754-A1.  
 XX  
 XX PD 17-OCT-2002.  
 XX  
 XX PF 04-APR-2002; 2002WO-US010764.  
 XX  
 XX PR 04-APR-2001; 2001US-00826115.  
 XX  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 XX PI Chang GJ;  
 XX  
 XX DR WPI; 2003-058572/05.  
 XX  
 XX DR Novel isolated nucleic acid useful as vaccine for preventing flavivirus  
 XX infection, comprises transcriptional unit encoding signal sequence of one  
 XX flavivirus and immunogenic flavivirus antigen of a second flavivirus.  
 XX  
 XX PS Example 15; Page 135-137; 174pp; English.  
 XX  
 XX CC The invention relates to a novel nucleic acid comprising a  
 XX transcriptional unit encoding a signal sequence of a structural protein  
 XX of a first flavivirus and an immunogenic flavivirus antigen of a second  
 XX flavivirus, where the transcriptional unit directs the synthesis of the  
 XX antigen. The polynucleotide of the invention has virucide activity, and  
 XX acts as a vaccine. A composition of the invention is useful for  
 XX immunising a subject against infection by a flavivirus. The  
 XX polynucleotide is useful as a vaccine for preventing flavivirus  
 XX infection. The sequence represents plasmid pCBPOW, which contains  
 XX Powassan virus prM and E encoding proteins. Note: The protein sequence is  
 XX not encoded by the cDNA sequence given in ABV77538, which is quoted as  
 XX the encoding polynucleotide in the specification  
 XX  
 XX SQ Sequence 681 AA;  
 XX  
 XX Query Match 81.4%; Score 96; DB 6; Length 681;  
 XX Best Local Similarity 87.5%; Pred. No. 7.3e-06;  
 XX Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 XX  
 XX QY 1 MGKRSAGSIMWLASLAVVIACAGA 24  
 XX |||||  
 XX Db 1 MGKRSAGSIMWLASLAVVIAGTSA 24  
 XX |||||  
 XX  
 XX RESULT 10  
 XX ABP57862  
 XX ID ABP57862 standard; protein; 692 AA.  
 XX  
 XX AC ABP57862;  
 XX  
 XX DT 07-FEB-2003 (first entry)  
 XX  
 XX DE Plasmid pCBJESS-M containing St. Louis encephalitis virus prM and E.  
 XX  
 XX KW Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;  
 XX pCBJESS-M; St. Louis encephalitis virus.  
 XX  
 XX OS Unidentified.  
 XX  
 XX OS St. Louis encephalitis virus.  
 XX Chimeric.  
 XX  
 XX PN WO200281754-A1.  
 XX  
 XX PD 17-OCT-2002.  
 XX  
 XX PF 04-APR-2002; 2002WO-US010764.  
 XX  
 XX PR 04-APR-2001; 2001US-00826115.  
 XX  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX

PI Chang GJ;  
 XX  
 XX DR WPI; 2003-058572/05.  
 XX  
 XX DR N-P5DB; ABV77539.  
 XX  
 XX PT Novel isolated nucleic acid useful as vaccine for preventing flavivirus  
 XX infection, comprises transcriptional unit encoding signal sequence of one  
 XX flavivirus and immunogenic flavivirus antigen of a second flavivirus.  
 XX  
 XX PS Example 13; Page 141-142; 174pp; English.  
 XX  
 XX CC The invention relates to a novel nucleic acid comprising a  
 XX transcriptional unit encoding a signal sequence of a structural protein  
 XX of a first flavivirus and an immunogenic flavivirus antigen of a second  
 XX flavivirus, where the transcriptional unit directs the synthesis of the  
 XX antigen. The polynucleotide of the invention has virucide activity, and  
 XX acts as a vaccine. A composition of the invention is useful for  
 XX immunising a subject against infection by a flavivirus. The  
 XX polynucleotide is useful as a vaccine for preventing flavivirus  
 XX infection. The sequence represents plasmid pCBJESS-M, which contains St.  
 XX Louis encephalitis virus prM and E proteins  
 XX  
 XX SQ Sequence 692 AA;  
 XX  
 XX Query Match 81.4%; Score 96; DB 6; Length 692;  
 XX Best Local Similarity 87.5%; Pred. No. 7.4e-06;  
 XX Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 XX  
 XX QY 1 MGKRSAGSIMWLASLAVVIACAGA 24  
 XX |||||  
 XX Db 1 MGKRSAGSIMWLASLAVVIAGTSA 24  
 XX |||||  
 XX  
 XX RESULT 11  
 XX ABP57879  
 XX ID ABP57879 standard; peptide; 39 AA.  
 XX  
 XX AC ABP57879;  
 XX  
 XX DT 07-FEB-2003 (first entry)  
 XX  
 XX DE Signal sequence preceding prM protein in plasmid pCBJES1-14.  
 XX  
 XX KW Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;  
 XX signal sequence.  
 XX  
 XX OS Unidentified.  
 XX  
 XX PN WO200281754-A1.  
 XX  
 XX PD 17-OCT-2002.  
 XX  
 XX PF 04-APR-2002; 2002WO-US010764.  
 XX  
 XX PR 04-APR-2001; 2001US-00826115.  
 XX  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 XX PI Chang GJ;  
 XX  
 XX DR WPI; 2003-058572/05.  
 XX  
 XX PT Novel isolated nucleic acid useful as vaccine for preventing flavivirus  
 XX infection, comprises transcriptional unit encoding signal sequence of one  
 XX flavivirus and immunogenic flavivirus antigen of a second flavivirus.  
 XX  
 XX PS Disclosure; Fig 6; 174pp; English.  
 XX  
 XX CC The invention relates to a novel nucleic acid comprising a  
 XX transcriptional unit encoding a signal sequence of a structural protein  
 XX of a first flavivirus and an immunogenic flavivirus antigen of a second  
 XX flavivirus, where the transcriptional unit directs the synthesis of the  
 XX antigen. The polynucleotide of the invention has virucide activity, and

Qy 1 MGKR-----SAGSIMWLASLAVVIACAGA 24

KW haemagglutination; beta-actin promoter; vaccine.

XX Japanese encephalitis virus.

XX JP2004065118-A.

PN 04-MAR-2004.

XX 07-AUG-2002; 2002JP-00229597.

XX 07-AUG-2002; 2002JP-00229597.

XX (HAND-) ZH HANDAI BISEIBUTSUBYO KENKYUKAI.  
PA (KOKU-) KOKURITSU YORO EISEI KENKYUSHO.

XX WPI: 2004-209123/20.

DR N-PSDB; ADM97133.

XX Novel Japanese-encephalitis-virus antigen comprising Japanese-

PT encephalitis-virus-like particle consisting of M and E protein, useful as  
PT Japanese-encephalitis vaccine.

XX Disclosure; SEQ ID NO 5; 45pp; Japanese.

CC The invention relates to a novel Japanese-encephalitis-virus antigen  
CC comprising a Japanese-encephalitis-virus-like particle, which includes  
CC the M protein and E protein of a Japanese encephalitis virus, and which  
CC does not contain RNA in the particle, and shows haemagglutination  
CC activity. The invention further comprises: a transformed cell obtained by  
CC providing cDNA encoding the E protein and prM protein prepared from the  
CC genome RNA of a Japanese-encephalitis virus, preparing a recombinant DNA  
CC by integrating the cDNA in an expression vector which contains a beta-  
CC actin promoter and which can be expressed, transforming an animal cell by  
CC the recombinant DNA, selecting the transformed cell from a parent cell  
CC and making the transformed cell to acclimatize in serum free medium;  
CC Japanese-encephalitis-vaccine having immunity for the novel antigen and  
CC containing the antigen as an active ingredient; and a diagnostic agent  
CC which contains the antigen as an active ingredient. The Japanese-  
CC encephalitis-virus antigen is useful for carrying out the preparation of  
CC a Japanese-encephalitis vaccine and a diagnostic agent. This sequence  
CC represents the Japanese-encephalitis-virus signal peptide of the  
CC invention.

XX Sequence 23 AA;

Query Match 75.4%; Score 89; DB 8; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.4e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GSIMWLASLAVVIACAGA 24

DB 6 GSIMWLASLAVVIACAGA 23

RESULT 15

ABP57867

ID ABP57867 standard; peptide; 30 AA.

XX AC ABP57867;

XX DT 07-FEB-2003 (first entry)

XX Signal sequence preceding prM protein in plasmid pCJEME.

XX Flavivirus; immunogenic flavivirus antigen; virucide; vaccine; prM-E;  
KW signal sequence.

XX Unidentified.

XX OS WO200281754-A1.

XX PN 17-OCT-2002.

XX PD

PF 04-APR-2002; 2002WO-US010764.

XX 04-APR-2001; 2001US-00826115.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Chang GJ;

XX WPI: 2003-058572/05.

XX Novel isolated nucleic acid useful as vaccine for preventing flavivirus  
PT infection, comprises transcriptional unit encoding signal sequence of one  
PT flavivirus and immunogenic flavivirus antigen of a second flavivirus.

XX Example 20; Page 87; 174pp; English.

CC The invention relates to a novel nucleic acid comprising a  
CC transcriptional unit encoding a signal sequence of a structural protein  
CC of a first flavivirus and an immunogenic flavivirus antigen of a second  
CC flavivirus, where the transcriptional unit directs the synthesis of the  
CC antigen. The polynucleotide of the invention has virucide activity, and  
CC acts as a vaccine. A composition of the invention is useful for  
CC immunising a subject against infection by a flavivirus. The  
CC polynucleotide is useful as a vaccine for preventing flavivirus  
CC infection. The sequence represents the signal sequence preceding the prM  
CC protein in the plasmid pCJEME of the invention

XX Sequence 30 AA;

Query Match 75.4%; Score 89; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 3.1e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GSIMWLASLAVVIACAGA 24

DB 4 GSIMWLASLAVVIACAGA 21

Search completed: October 26, 2005, 01:31:37  
Job time : 167 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 26, 2005, 01:23:39 ; Search time 38 Seconds  
(without alignments)  
60.768 Million cell updates/sec

Title: US-09-826-115a-14  
Perfect score: 118  
Sequence: 1 MGKRSAGSIMVLASLAVVIACAGA 24

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	75.4	789	2 I50804	polyprotein - Japa
2	89	75.4	1440	1 GNVVJF	genome polyprotein
3	89	75.4	3432	1 GNVVJS	genome polyprotein
4	78	66.1	3432	1 GNVVJE	genome polyprotein
5	53	44.9	354	2 AF3614	probable undecapre
6	53	44.9	385	2 A91006	probable transport
7	53	44.9	385	2 B85850	probable transport
8	52	44.1	891	2 G96636	hypothetical prote
9	51	43.2	485	2 H82822	NADH-ubiquinone ox
10	50	42.4	299	2 T34987	probable integral
11	50	42.4	385	2 A64981	Yehy protein - Esc
12	49	41.5	203	2 H71346	hypothetical prote
13	49	41.5	204	2 C97866	hypothetical prote
14	48	40.7	485	2 D65118	panthothenate perme
15	48	40.7	485	2 F85990	sodium/pantothemat
16	48	40.7	485	2 B91145	sodium/pantothemat
17	48	40.7	506	2 AD1119	Flavocytochrome C
18	48	40.7	628	2 T02602	vacuolar sorting r
19	47	39.8	171	2 H64107	signal peptidase I
20	47	39.8	210	2 I51084	prolactin precursor
21	47	39.8	210	2 PNO092	prolactin precursor
22	47	39.8	210	2 A31364	prolactin precursor
23	47	39.8	210	2 S52475	prolactin - Atlant
24	47	39.8	210	2 S34351	prolactin precursor
25	47	39.8	211	2 S00359	prolactin precursor
26	47	39.8	483	2 AC0913	sodium/pantothemat
27	47	39.8	506	2 AG1479	Flavocytochrome C
28	46.5	39.4	225	2 A90260	conserved hypothet
29	46.5	39.4	491	2 AG0557	AmpG protein [impo

30	46.5	39.4	491	2 G90689	regulates beta-lac
31	46.5	39.4	491	2 C85540	regulates beta-lac
32	46.5	39.4	491	2 S37391	signal transducer
33	46	39.0	173	2 F87521	hypothetical prote
34	46	39.0	239	2 F82717	30S ribosomal prot
35	46	39.0	315	2 H70800	probable secretedp
36	46	39.0	336	2 A47542	short-chain alcoh
37	46	39.0	476	2 A83387	probable transport
38	46	39.0	484	2 AB0445	sodium/pantothemat
39	46	39.0	509	2 T48168	hypothetical prote
40	46	39.0	650	2 T17482	ABC-type transport
41	46	39.0	727	2 I56506	Na+/Cl(-)-dependen
42	45	38.1	185	2 A70682	hypothetical prote
43	45	38.1	200	2 B83642	hypothetical prote
44	45	38.1	226	2 E70501	probable transmem
45	45	38.1	252	2 A69096	nitrogenase reduct

## ALIGNMENTS

### RESULT 1

I50804  
polyprotein - Japanese encephalitis virus (fragment)  
C:Species: Japanese encephalitis virus  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: I50804

R.Ni, H.; Barrett, A.D.

J. Gen. Virol. 76, 401-407, 1995

A:Title: Nucleotide and deduced amino acid sequence of the structural protein genes of J2

A:Reference number: I50804; MUID:95146981; PMID:7844559

A:Accession: I50804

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-789 <NIX>

A:Cross-references: UNIPROT:Q82865; EMBL:U03693; NID:G517403; PIDN:AAA67162.1; PID:G51740

C:Superfamily: Yellow fever virus genome polyprotein

C:Keywords: polyprotein

Query Match 75.4%; Score 89; DB 2; Length 789;  
Best Local Similarity 100.0%; Pred. No. 3.9e-05;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSIMVLASLAVVIACAGA 24  
DB 110 GSIMVLASLAVVIACAGA 127

### RESULT 2

GNVVJF

genome polyprotein - Japanese encephalitis virus (strain Nakayama) (fragment)  
N:Contains: amino end of nonstructural protein NS3; carboxyl end of capsid protein C; en  
ein NS2b

C:Species: Japanese encephalitis virus

C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 09-Jul-2004

C:Accession: A27844

R:McAda, P.C.; Mason, P.W.; Schmaljohn, C.S.; Dalrymple, J.M.; Mason, T.L.; Fournier, M.

Virology 158, 348-360, 1987

A:Title: Partial nucleotide sequence of the Japanese encephalitis virus genome.

A:Reference number: A27844; MUID:87236200; PMID:3035787

A:Accession: A27844

A:Molecule type: genomic RNA

A:Residues: 1-1440 <MCA>

A:Cross-references: UNIPROT:P14403; GB:M16574; NID:G331336; PIDN:AAA46251.1; PID:G331337

C:Superfamily: Yellow fever virus genome polyprotein

C:Keywords: capsid protein; envelope protein; glycoprotein; membrane protein; nonstructu

F:1-53/Product: capsid protein C #status predicted <CPC>

F:54-222/Product: membrane protein M precursor #status predicted <MPP>

F:54-146/Domain: nonterminal signal sequence #status predicted <SIG>

F:147-222/Product: membrane protein M #status predicted <MEP>

F:223-722/Product: envelope protein E #status predicted <EPE>

F:723-1136/Product: nonstructural protein NS1 #status predicted <NS1>

F:1137-1301/Product: nonstructural protein NS2a #status predicted <N2a>

F:1302-1432/Product: nonstructural protein NS2b #status predicted <N2B>  
 F:1433-1440/Product: nonstructural protein NS3 (fragment) #status predicted <NS3>  
 F:68,80,376,852,929/Binding site: carbohydrate (Asn) #status predicted

Query Match 75.4%; Score 89; DB 1; Length 1440;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-05; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; Mismatches 0

QY 7 GSIMWLASLAVVIACAGA 24  
 |||||  
 DB 36 GSIMWLASLAVVIACAGA 53

RESULT 3  
 GNMVJS  
 genome polypeptide - Japanese encephalitis virus (strain SA-14)  
 N:Contains: capsid protein; envelope protein; membrane protein; nonstructural protein NS  
 a; nonstructural protein NS4b; nonstructural protein NS5  
 C:Species: Japanese encephalitis virus  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 19-Jan-2001  
 C:Accession: A35519  
 R:Nitayaphan, S.; Grant, J.A.; Chang, G.J.-J.; Trent, D.W.  
 Virology 177, 541-552, 1990  
 A:Title: Nucleotide sequence of the virulent SA-14 strain of Japanese encephalitis virus  
 A:Reference number: A35519; MUID:90320126; PMD:2371768  
 A:Accession: A35519  
 A:Molecule type: genomic RNA  
 A:Residues: 1-3432 <NT>  
 C:Superfamily: yellow fever virus genome polypeptide  
 C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;  
 F:1-127/Product: capsid protein #status predicted <CAP>  
 F:46-67/Domain: transmembrane #status predicted <TN1>  
 F:110-127/Domain: transmembrane #status predicted <TN2>  
 F:128-294/Product: membrane protein I precursor #status predicted <GLC>  
 F:128-219/Domain: nonterminal signal sequence #status predicted <SIG>  
 F:220-294/Product: membrane protein II #status predicted <GLM>  
 F:280-294/Domain: transmembrane #status predicted <TN3>  
 F:295-794/Product: envelope protein #status predicted <ENV>  
 F:745-767/Domain: transmembrane #status predicted <TN4>  
 F:774-792/Domain: transmembrane #status predicted <TN5>  
 F:795-1206/Product: nonstructural protein NS1 #status predicted <NS1>  
 F:1178-1197/Domain: transmembrane #status predicted <TN6>  
 F:1207-1373/Product: nonstructural protein NS2a #status predicted <N2A>  
 F:1374-1504/Product: nonstructural protein NS2b #status predicted <N2B>  
 F:1505-2123/Product: nonstructural protein NS3 #status predicted <NS3>  
 F:1698-1705/Region: nucleotide-binding motif A (P-loop)  
 F:1785-1790/Region: nucleotide-binding motif B  
 F:1789-1792/Region: DEAH motif  
 F:2124-2412/Product: nonstructural protein NS4a #status predicted <N4A>  
 F:2413-2527/Product: nonstructural protein NS4b #status predicted <N4B>  
 F:2528-3432/Product: nonstructural protein NS5 #status predicted <NS5>  
 F:142,448,924,1001,1594,1950,2463,2491,2761,2866,2904/Binding site: carbohydrate (Asn)

Query Match 75.4%; Score 89; DB 1; Length 3432;  
 Best Local Similarity 100.0%; Pred. No. 0.00013; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; Mismatches 0

QY 7 GSIMWLASLAVVIACAGA 24  
 |||||  
 DB 110 GSIMWLASLAVVIACAGA 127

RESULT 4  
 GNMVJE  
 genome polypeptide - Japanese encephalitis virus (strain JAORs982 wild type)  
 N:Contains: capsid protein C; envelope protein E; membrane protein M; nonstructural pro  
 in NS4a; nonstructural protein NS4b; nonstructural protein NS5  
 C:Species: Japanese encephalitis virus  
 C:Date: 30-Jun-1988 #sequence\_revision 30-Sep-1989 #text\_change 09-Jul-2004  
 C:Accession: A27403; A48387; A26465  
 R:Sumiyoshi, H.; Mori, C.; Fuke, I.; Morita, K.; Kuhara, S.; Kondou, J.; Kikuchi, Y.; Na  
 Virology 161, 497-510, 1987

A:Title: Complete nucleotide sequence of the Japanese encephalitis virus genome RNA.  
 A:Reference number: A94367; MUID:88072090; PMD:3686827  
 A:Accession: A27403  
 A:Molecule type: genomic RNA  
 A:Residues: 1-3432 <SUM>  
 A:Cross-references: UNIPROT:P32886; GB:M18370; NID:G331329; PIDN:AAA81554.1; PID:G331330  
 R:Chen, W.R.; Rico-Hesse, R.; Tesh, R.B.  
 Am. J. Trop. Med. Hyg. 47, 61-69, 1992  
 A:Title: A new genotype of Japanese encephalitis virus from Indonesia.  
 A:Reference number: A48387; MUID:92344001; PMD:1322071  
 A:Accession: A48387  
 A:Molecule type: genomic RNA  
 A:Residues: 121-200 <CHE>  
 A:Experimental source: isolate JAORs982  
 A:Note: sequence extracted from NCBI backbone (NCBIN:109245, NCBIP:109246)  
 C:Superfamily: yellow fever virus genome polypeptide  
 C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein; r  
 F:2-127/Product: capsid protein C #status predicted <CAP>  
 F:44-60/Domain: transmembrane #status predicted <TN1>  
 F:112-127/Domain: transmembrane #status predicted <TN2>  
 F:128-294/Product: membrane protein M precursor #status predicted <GLC>  
 F:128-219/Domain: nonterminal signal sequence #status predicted <SIG>  
 F:220-294/Product: membrane protein M #status predicted <GLM>  
 F:280-294/Domain: transmembrane #status predicted <TN3>  
 F:295-794/Product: envelope protein E #status predicted <ENV>  
 F:774-790/Domain: transmembrane #status predicted <TN4>  
 F:795-1206/Product: nonstructural protein NS1 #status predicted <NS1>  
 F:1207-1373/Product: nonstructural protein NS2a #status predicted <N2A>  
 F:1374-1504/Product: nonstructural protein NS2b #status predicted <N2B>  
 F:1505-2123/Product: nonstructural protein NS3 #status predicted <NS3>  
 F:1698-1705/Region: nucleotide-binding motif A (P-loop)  
 F:1785-1790/Region: nucleotide-binding motif B  
 F:1789-1792/Region: DEAH motif  
 F:2124-2412/Product: nonstructural protein NS4a #status predicted <N4A>  
 F:2413-2527/Product: nonstructural protein NS4b #status predicted <N4B>  
 F:2528-3432/Product: nonstructural protein NS5 #status predicted <NS5>  
 F:142,448,924,1001,1594,1950,2463,2491,2761,2866,2904/Binding site: carbohydrate (Asn)

Query Match 66.1%; Score 78; DB 1; Length 3432;  
 Best Local Similarity 94.4%; Pred. No. 0.0051;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GSIMWLASLAVVIACAGA 24  
 |||||  
 DB 110 GSIMWLASLAVVIACAGA 127

RESULT 5  
 AF3614  
 Probable undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase (EC 2.4.1.-) [impor  
 C:Species: Brucella melitensis  
 C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
 C:Accession: AF3614  
 R:DelVecchio, V.G.; Kaputal, V.; Redkar, R.J.; Patra, G.; Mujter, C.; Los, T.; Ivanova, I  
 ; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc  
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
 A:Reference number: AD3252; PMD:11756688  
 A:Accession: AF3614  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-354 <KUR>  
 A:Cross-references: UNIPROT:Q8YBQ5; GB:AE008918; PIDN:AAL54081.1; PID:G17985038; GSPDB:GN  
 A:Experimental source: strain 16M  
 C:Genetics:  
 A:Gene: BMEII0839  
 A:Map position: 11  
 C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 44.9%; Score 53; DB 2; Length 354;  
 Best Local Similarity 38.9%; Pred. No. 3.5;  
 Matches 14; Conservative 1; Mismatches 7; Indels 14; Gaps 1;

QY 2 GKRSAGSIMWLA-----SLAVVIACAG 23  
 Db 153 GSASASFWLAVISFDIGCEHRLGLQSLALVACLG 188

RESULT 6  
 A:Accession: A91006  
 C:Species: Escherichia coli  
 C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
 C:Accession: A91006  
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
 Gasaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic  
 A:Reference number: A99629; MUID:21156231; PMID:11258796  
 A:Accession: A91006  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-385 <HAY>  
 A:Cross-references: UNIPROT:O8X670; GB:BA000007; PIDN:BA036440.1; PID:gl3362486; GSPDB:G  
 A:Experimental source: strain O157:H7, substrain RMD 0509952  
 C:Genetics:  
 A:Gene: ECS3017

Query Match 44.9%; Score 53; DB 2; Length 385;  
 Best Local Similarity 41.7%; Pred. No. 3.7;  
 Matches 10; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 MKGRSAGSIMWLASLAVVIACAGA 24  
 Db 103 LARTSLGSGFWLASLALLACSDA 126

RESULT 7  
 B85850  
 C:Species: Escherichia coli  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
 C:Accession: B85850  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: B85850  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-385 <STO>  
 A:Cross-references: UNIPROT:O8X670; GB:AE005174; NID:gl2516435; PIDN:AAG57262.1; GSPDB:G  
 A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: yehy

Query Match 44.9%; Score 53; DB 2; Length 385;  
 Best Local Similarity 41.7%; Pred. No. 3.7;  
 Matches 10; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 MKGRSAGSIMWLASLAVVIACAGA 24  
 Db 103 LARTSLGSGFWLASLALLACSDA 126

RESULT 8  
 G96636  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C:Accession: G96636  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
 ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712  
 A:Accession: G96636  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-891 <STO>  
 A:Cross-references: UNIPROT:O22735; GB:AE005173; NID:g2443891; PIDN:AAB71484.1; GSPDB:GN  
 C:Genetics:  
 A:Gene: Flp17.17  
 A:Map position: 1

Query Match 44.1%; Score 52; DB 2; Length 891;  
 Best Local Similarity 50.0%; Pred. No. 10;  
 Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 3 KRSAGSIMWLASLAVVIACAGA 22  
 Db 302 KKHGDLGLWMAELAAVAKACA 321

RESULT 9  
 H82822  
 A:Title: NADH-ubiquinone oxidoreductase, NQO14 subunit XF0318 [imported] - Xylella fastidiosa (str  
 C:Species: Xylella fastidiosa  
 C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
 C:Accession: H82822  
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc  
 Nature 406, 151-157, 2000  
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A:Reference number: A82515; MUID:20365717; PMID:10910347  
 A:Note: for a complete list of authors see reference number A59328 below  
 A:Accession: H82822  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-485 <SIM>  
 A:Cross-references: UNIPROT:Q9PGI2; GB:AE003884; GB:AE003849; NID:g9105127; PIDN:AAF8312;  
 A:Experimental source: strain 945C  
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; AJ  
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carraro, D.M.; Carreir, H.  
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facinani, A.P.; Ferreira, A.J.S.  
 submitted to GenBank, June 2000  
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme  
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.B.; Laigre  
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.  
 A:Authors: Martins, E.M.F.; Matukuma, A.V.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.  
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasakj  
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
 M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
 A:Reference number: A59328  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: XF0318  
 C:Superfamily: NADH dehydrogenase (ubiquinone) chain 2

Query Match 43.2%; Score 51; DB 2; Length 485;  
 Best Local Similarity 41.7%; Pred. No. 8.8;  
 Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 MKRSAGSIMWLASLAVVIACAGA 24  
 Db 401 LGAAVQGGMLWLAIGVCAVIGA 424

RESULT 10  
 T34987  
 C:Species: Streptomyces coelicolor

```
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C/Accession: T34987
R:Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A/Reference number: Z21550
A/Accession: T34987
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-299 <OLI>
A/Cross-references: UNIPROT:O86668; EMBL:AL031182; PIDN:CAA20164.1; GSPDB:GN00070; SCOE
A/Experimental source: strain A3(2)
C/Genetics:
A/Gene: SCOEDB:SC4R2.12

Query Match      42.4%; Score 50; DB 2; Length 299;
Best Local Similarity 41.7%; Pred. No. 8.3;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY      1  MGKRSAGSIMWLASLAVVIACAGA 24
Db      238  LGDRPRSGLWLAAGVFAAVAGA 261

RESULT 11
A64981
yehY protein - Escherichia coli (strain K-12)
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C/Accession: A64981
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: A64981
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-385 <BLAT>
A/Cross-references: UNIPROT:P33361; GB:AE000302; GB:U00096; NID:g1788447; PIDN:AAC75191.
A/Experimental source: strain K-12, substrain MG1655
C/Genetics:
A/Gene: yehY

Query Match      42.4%; Score 50; DB 2; Length 385;
Best Local Similarity 37.5%; Pred. No. 10;
Matches 9; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY      1  MGKRSAGSIMWLASLAVVIACAGA 24
Db      103  LARTSLGSGFWLAAALALACSDA 126

RESULT 12
H71346
hypothetical protein TP0259 - syphilis spirochete
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: H71346
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwir
ron, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A/Reference number: A71250; MUID:98332770; PMID:9665876
A/Accession: H71346
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-203 <COL>
A/Cross-references: UNIPROT:O83283; GB:AE001207; GB:AE000520; NID:g3322526; PIDN:AAC6525
A/Experimental source: strain Nichols
C/Genetics:
A/Gene: TP0259
C/Superfamily: syphilis spirochete hypothetical protein TP0259
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```
Query Match      41.5%; Score 49; DB 2; Length 203;
Best Local Similarity 37.5%; Pred. No. 8.4;
Matches 9; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY      1  MGKRSAGSIMWLASLAVVIACAGA 24
Db      30  MKKLSTGLLWIAFISGVTCKSA 53

RESULT 13
C97866
hypothetical protein RC1331 [imported] - Rickettsia conorii (strain Malish 7)
C/Species: Rickettsia conorii
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C/Accession: C97866
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A/Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A/Reference number: A97700; MUID:21442074; PMID:11557893
A/Accession: C97866
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-204 <KUR>
A/Cross-references: UNIPROT:Q92FZ6; GB:AE006914; PIDN:AAL03869.1; PID:g15620473; GSPDB:G
C/Genetics:
A/Gene: RC1331

Query Match      41.5%; Score 49; DB 2; Length 204;
Best Local Similarity 31.7%; Pred. No. 8.5;
Matches 13; Conservative 5; Mismatches 5; Indels 18; Gaps 1;

QY      2  GKRSAGSIMWLAS-----LAVVIACAGA 24
Db      131  GKSIAGSITFLASAFISILVVFVLYGNTSFIIIIICIGA 171

RESULT 14
D65118
pantothenate permease [validated] - Escherichia coli (strain K-12)
N/Alternate names: sodium/pantothenate symporter
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C/Accession: D65118; JU0296; A49924
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: D65118
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-485 <BLAT>
A/Cross-references: UNIPROT:O8X9B1; GB:AE000404; GB:U00096; NID:g2367207; PIDN:AAC76290.1
A/Experimental source: strain K-12, substrain MG1655
R:Jackowski, S.; Alix, J.H.
J. Bacteriol. 172, 3842-3848, 1990
A/Title: Cloning, sequence, and expression of the pantothenate permease (panF) gene of E
A/Reference number: JU0296; MUID:90299808; PMID:12193919
A/Accession: JU0296
A/Molecule type: DNA
A/Residues: 3-180, 'APAAERH', 207-208, 'RACDADWRCAYWSTC', 209-255, 'A', 257-303, 'H', 305-485
A/Cross-references: GB:M30953; NID:g147066; PIDN:AAA24276.1; PID:g147067
A/Experimental source: strain K32
R:Vanet, A.; Plumbbridge, J.A.; Alix, J.H.
J. Bacteriol. 175, 7178-7188, 1993
A/Title: Corranscription of two genes necessary for ribosomal protein L11 methylation (p
A/Reference number: A49924; MUID:94042890; PMID:8226664
A/Accession: A49924
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 445-485 <VAN>
A/Cross-references: GB:S67010; NID:g455653; PIDN:AAB28768.1; PID:g455654
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A:Experimental source: strain K12  
 A:Note: sequence extracted from NCBI backbone (NCBIN:139766, NCBIP:139767)  
 C:Genetics:  
 A:Gene: panF  
 C:Function:

A:Description: catalyzes the sodium-dependent uptake of extracellular pantothenate (valid)  
 C:Superfamily: proline carrier protein  
 C:Keywords: sodium transport; symport system; transmembrane protein

Query Match 40.7%; Score 48; DB 2; Length 485;

Best Local Similarity 50.0%; Pred. No. 24;

Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 9 IMWLASLAVVIACAGA 24

Db 125 LVWLASLSLLVAFVGA 140

# RESULT 15

F85990

sodium/pantothenate symporter [imported] - Escherichia coli (strain O157:H7, substrain E

C:Species: Escherichia coli

C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

C:Accession: F85990

R:Perla, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
 Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: AB5480; MUID:21074935; PMID:11206551

A:Accession: F85990

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-485 <STO>

A:Cross-References: UNIPROT:Q8X9B1; GB:AB005174; NID:G12517885; PIDN:AGS8386.1; GSPDB:C  
 A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: panF

C:Superfamily: proline carrier protein

Query Match 40.7%; Score 48; DB 2; Length 485;

Best Local Similarity 50.0%; Pred. No. 24;

Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 9 IMWLASLAVVIACAGA 24

Db 125 LVWLASLSLLVAFVGA 140

Search completed: October 26, 2005, 01:35:14

Job time : 40 secs

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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 01:15:29 ; Search time 169 Seconds  
(without alignments)  
72.721 Million cell updates/sec

Title: US-09-826-115A-14  
Perfect score: 118  
Sequence: 1 MGRSAGSIMMLASLAVIACAGA 24

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	76.3	789	2 Q82863	Q82863 Japanese en
2	89	75.4	789	2 Q82860	Q82860 Japanese en
3	89	75.4	789	2 Q82862	Q82862 Japanese en
4	89	75.4	789	2 Q82865	Q82865 Japanese en
5	89	75.4	789	2 Q82866	Q82866 Japanese en
6	89	75.4	789	2 Q82868	Q82868 Japanese en
7	89	75.4	789	2 Q82874	Q82874 Japanese en
8	89	75.4	793	2 Q82862	Q82862 Japanese en
9	89	75.4	794	2 Q82869	Q82869 Japanese en
10	89	75.4	794	2 Q82870	Q82870 Japanese en
11	89	75.4	1437	2 Q82862	Q82862 Japanese en
12	89	75.4	1440	1 POLG_JAEVN	P14403 Japanese po
13	89	75.4	1504	2 Q4092	Q4092 Japanese po
14	89	75.4	3432	1 POLG_JAEV1	P27395 Japanese po
15	89	75.4	3432	1 POLG_JAEV5	P19110 Japanese po
16	89	75.4	3432	2 Q36764	Q36764 Japanese en
17	89	75.4	3432	2 Q36765	Q36765 Japanese en
18	89	75.4	3432	2 Q4091	Q4091 Japanese en
19	89	75.4	3432	2 Q8JZH8	Q8JZH8 Japanese en
20	89	75.4	3432	2 Q8JZH9	Q8JZH9 Japanese en
21	89	75.4	3432	2 Q8QD0	Q8QD0 Japanese en
22	89	75.4	3432	2 Q917U0	Q917U0 Japanese en
23	89	75.4	3432	2 Q99DQ9	Q99DQ9 Japanese en
24	89	75.4	3432	2 Q6JV19	Q6JV19 Japanese en
25	89	75.4	3432	2 Q6JV20	Q6JV20 Japanese en
26	89	75.4	3432	2 Q82872	Q82872 Japanese en
27	89	75.4	3432	2 Q82873	Q82873 Japanese en
28	89	75.4	3432	2 Q9WBS5	Q9WBS5 Japanese en
29	89	75.4	3432	2 Q9WCX5	Q9WCX5 Japanese en
30	89	75.4	3432	2 Q9WCX6	Q9WCX6 Japanese en
31	89	75.4	3432	2 Q9WCX7	Q9WCX7 Japanese en

```
32 87 73.7 576 2 Q8QSF1 Japanese en
33 86 72.9 3432 2 Q91JX6 Japanese en
34 85 72.0 789 2 Q82867 Japanese en
35 85 72.0 1173 2 Q8JQ48 Japanese en
36 85 72.0 3432 2 Q90297 Japanese en
37 85 72.0 3432 2 Q6PR34 Japanese en
38 85 72.0 3432 2 Q82919 Japanese en
39 84 71.2 3432 2 Q90417 Japanese en
40 84 71.2 3432 2 Q8QXP6 Japanese en
41 83 70.3 789 2 Q82875 Japanese en
42 81 68.6 789 2 Q82861 Japanese en
43 78 66.1 789 2 Q82864 Japanese en
44 78 66.1 3432 1 POLG_JAEVJ genome po
45 77 65.3 3432 2 Q6JV17 Japanese en
```

## ALIGNMENTS

```
RESULT 1
Q82863 PRELIMINARY; PRT; 789 AA.
AC Q82863;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Polyprotein (Fragment).
OS Japanese encephalitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
NC NCBI_TaxID=11072;
RX STRAIN=8256; PubMed=7844559;
RA Ni H., Barrett A.D.;
RT "Nucleotide and deduced amino acid sequence of the structural protein
RT genes of a Japanese encephalitis viruses from different geographical
RT locations";
RL J. Gen. Virol. 76:401-407 (1995).
DR EMBL; U03691; AAA67160.1; -.
DR HSP; Q88653; IOKE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0019058; P:viral infectious cycle; IEA.
DR InterPro; IPR001122; Flavi_capsidC.
DR InterPro; IPR000336; Flavi_glycoprote.
DR InterPro; IPR000069; Flavi_M.
DR InterPro; IPR002535; Flavi_propep.
DR Pfam; PF01003; Flavi_capsid; 1.
DR Pfam; PF00869; Flavi_glycoprote; 1.
DR Pfam; PF02832; Flavi_glycoprote; 1.
DR Pfam; PF01004; Flavi_M; 1.
DR ProDom; PD001570; Flavi_propep; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
KW Polyprotein.
FT NON_TER 789
SQ SEQUENCE 789 AA; 85517 MW; E0DC176FDA561636 CRC64;
```

Query Match 76.3%; Score 90; DB 2; Length 789;  
Best Local Similarity 90.0%; Pred. No. 0.00014;  
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SAGSIMMLASLAVIACAGA 24  
: |||||  
Db 108 NGGSIMMLASLAVIACAGA 127

```
RESULT 2
Q82860 PRELIMINARY; PRT; 789 AA.
AC Q82860;
```

DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-WAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE Polyprotein (Fragment).  
 OS Japanese encephalitis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Flavivirus  
 OX NCBI\_TaxID=11072;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SA14-2-8;  
 RX MEDLINE=94267439; PubMed=8207417;  
 RA Ni H., Burns N.J., Chang G.J., Zhang M.J., Willis M.R., Trent D.W.,  
 RA Sanders P.G., Barrett A.D.;  
 RT "Comparison of nucleotide and deduced amino acid sequence of the 5'  
 RT non-coding region and structural protein genes of the wild-type  
 RT Japanese encephalitis virus strain SA14 and its attenuated vaccine  
 RT derivatives.";  
 RL J. Gen. Virol. 75:1505-1510(1994).  
 DR EMBL; U02367; AAA52215.1; -.  
 DR HSP; Q88653; IOKE.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR GO; GO:0019058; F:viral infectious cycle; IEA.  
 DR InterPro; IPR001122; Flavi\_capsidC.  
 DR InterPro; IPR000336; Flavi\_glycoproteE.  
 DR InterPro; IPR002535; Flavi\_propep.  
 DR Pfam; PF01003; Flavi\_capsid; 1.  
 DR Pfam; PF00869; Flavi\_glycoprot; 1.  
 DR Pfam; PF02832; Flavi\_glycop\_C; 1.  
 DR Pfam; PF01004; Flavi\_M; 1.  
 DR Pfam; PF01570; Flavi\_propep; 1.  
 DR ProDom; PD001556; Flavi\_glycoprote; 1.  
 KW Polyprotein. 789 789  
 FT NON\_TER  
 SQ SEQUENCE 789 AA; 85592 MW; 1A61502D9B53068E CRC64;

Query Match 75.4%; Score 89; DB 2; Length 789;  
 Best Local Similarity 100.0%; Pred. No. 0.0002;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSIMWLASLAVVIACAGA 24  
 |||||  
 DB 110 GSIMWLASLAVVIACAGA 127

RESULT 3  
 Q82862 ID Q82862 PRELIMINARY; PRT; 789 AA.  
 AC Q82862;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-WAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE Polyprotein (Fragment).  
 OS Japanese encephalitis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Flavivirus.  
 OX NCBI\_TaxID=11072;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DH20;  
 RX MEDLINE=95146981; PubMed=7844559;  
 RA Ni H., Barrett A.D.;  
 RT "Nucleotide and deduced amino acid sequence of the structural protein  
 RT genes of Japanese encephalitis viruses from different geographical  
 RT locations.";  
 RL J. Gen. Virol. 76:401-407(1995).  
 DR EMBL; U03690; AAA67159.1; -.  
 DR HSP; Q88653; IOKE.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR GO; GO:0019058; F:viral infectious cycle; IEA.  
 DR InterPro; IPR001122; Flavi\_capsidC.  
 DR InterPro; IPR000336; Flavi\_glycoproteE.  
 DR InterPro; IPR000069; Flavi\_M.  
 DR InterPro; IPR002535; Flavi\_propep.  
 DR Pfam; PF01003; Flavi\_capsid; 1.  
 DR Pfam; PF00869; Flavi\_glycoprot; 1.  
 DR Pfam; PF02832; Flavi\_glycop\_C; 1.  
 DR Pfam; PF01004; Flavi\_M; 1.  
 DR Pfam; PF01570; Flavi\_propep; 1.  
 DR ProDom; PD001556; Flavi\_glycoprote; 1.  
 KW Polyprotein. 789 789  
 FT NON\_TER  
 SQ SEQUENCE 789 AA; 85842 MW; C065C3905F12C051 CRC64;

Query Match 75.4%; Score 89; DB 2; Length 789;  
 Best Local Similarity 100.0%; Pred. No. 0.0002;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSIMWLASLAVVIACAGA 24  
 |||||  
 DB 110 GSIMWLASLAVVIACAGA 127

RESULT 4  
 Q82865 ID Q82865 PRELIMINARY; PRT; 789 AA.  
 AC Q82865;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-WAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE Polyprotein (Fragment).  
 OS Japanese encephalitis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Flavivirus.  
 OX NCBI\_TaxID=11072;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KPO34-35CT;  
 RX MEDLINE=95146981; PubMed=7844559;  
 RA Ni H., Barrett A.D.;  
 RT "Nucleotide and deduced amino acid sequence of the structural protein  
 RT genes of Japanese encephalitis viruses from different geographical  
 RT locations.";  
 RL J. Gen. Virol. 76:401-407(1995).  
 DR EMBL; U03693; AAA67162.1; -.  
 DR PIR; I50804; I50804.  
 DR HSP; Q88653; IOKE.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR GO; GO:0019058; F:viral infectious cycle; IEA.  
 DR InterPro; IPR001122; Flavi\_capsidC.  
 DR InterPro; IPR000336; Flavi\_glycoproteE.  
 DR InterPro; IPR000069; Flavi\_M.  
 DR InterPro; IPR002535; Flavi\_propep.  
 DR Pfam; PF01003; Flavi\_capsid; 1.  
 DR Pfam; PF00869; Flavi\_glycoprot; 1.  
 DR Pfam; PF02832; Flavi\_glycop\_C; 1.  
 DR Pfam; PF01004; Flavi\_M; 1.  
 DR Pfam; PF01570; Flavi\_propep; 1.  
 DR ProDom; PD001556; Flavi\_glycoprote; 1.  
 KW Polyprotein.  
 FT NON\_TER

Query Match 75.4%; Score 89; DB 2; Length 789;  
 Best Local Similarity 100.0%; Pred. No. 0.0002;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSIMWLASLAVVIACAGA 24  
 |||||

DB 110 GSIMMLASLAVVIACAGA 127

RESULT 5

Q82866 PRELIMINARY; PRT; 789 AA.

AC Q82866;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Polyprotein (fragment).

OS Japanese encephalitis virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Flavivirus.

OX NCBI\_TaxID=11072;

RN [1]\_

RP SEQUENCE FROM N.A.

RC STRAIN=Nakayama;

RX MEDLINE=95146981; PubMed=7844559;

RA Ni H., Barrett A.D.;

RT "Nucleotide and deduced amino acid sequence of the structural protein genes of Japanese encephalitis viruses from different geographical locations.";

RT J. Gen. Virol. 76:401-407 (1995).

DR EMBL; U03694; AAA67163.1; -.

DR HSP; Q88653; IOKE.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR GO; GO:0019058; P:viral infectious cycle; IEA.

DR InterPro; IPR001122; Flavi\_capsidC.

DR InterPro; IPR000336; Flavi\_glycoprote.

DR InterPro; IPR000069; Flavi\_M.

DR InterPro; IPR002535; Flavi\_propep.

DR Pfam; PF01003; Flavi\_capsid; 1.

DR Pfam; PF00869; Flavi\_glycoprot; 1.

DR Pfam; PF02832; Flavi\_glycop\_C; 1.

DR Pfam; PF01004; Flavi\_M; 1.

DR Pfam; PF01570; Flavi\_propep; 1.

DR ProDom; PD001556; Flavi\_glycoprote; 1.

KW Polyprotein.

FT NON\_TER

SQ SEQUENCE 789 AA; 85642 MW; 1B63A2A7F9FCB53D CRC64;

Query Match 75.4%; Score 89; DB 2; Length 789;

Best Local Similarity 100.0%; Pred. No. 0.0002;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSIMMLASLAVVIACAGA 24

DB 110 GSIMMLASLAVVIACAGA 127

RESULT 6

Q82868 PRELIMINARY; PRT; 789 AA.

AC Q82868;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Polyprotein (fragment).

OS Japanese encephalitis virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Flavivirus.

OX NCBI\_TaxID=11072;

RN [1]\_

RP SEQUENCE FROM N.A.

RC STRAIN=Saigon;

RX MEDLINE=95146981; PubMed=7844559;

RA Ni H., Barrett A.D.;

RT "Nucleotide and deduced amino acid sequence of the structural protein genes of Japanese encephalitis viruses from different geographical locations.";

RT J. Gen. Virol. 76:401-407 (1995).

DR EMBL; U03694; AAA67163.1; -.

DR HSP; Q88653; IOKE.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR GO; GO:0019058; P:viral infectious cycle; IEA.

DR InterPro; IPR001122; Flavi\_capsidC.

DR InterPro; IPR000336; Flavi\_glycoprote.

DR InterPro; IPR000069; Flavi\_M.

DR InterPro; IPR002535; Flavi\_propep.

DR Pfam; PF01003; Flavi\_capsid; 1.

DR Pfam; PF00869; Flavi\_glycoprot; 1.

DR Pfam; PF02832; Flavi\_glycop\_C; 1.

DR Pfam; PF01004; Flavi\_M; 1.

DR Pfam; PF01570; Flavi\_propep; 1.

DR ProDom; PD001556; Flavi\_glycoprote; 1.

KW Polyprotein.

FT NON\_TER

SQ SEQUENCE 789 AA; 85642 MW; 1B63A2A7F9FCB53D CRC64;

Query Match 75.4%; Score 89; DB 2; Length 789;

Best Local Similarity 100.0%; Pred. No. 0.0002;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSIMMLASLAVVIACAGA 24

DB 110 GSIMMLASLAVVIACAGA 127

RESULT 7

Q82874 PRELIMINARY; PRT; 789 AA.

AC Q82874;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Polyprotein (fragment).

OS Japanese encephalitis virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Flavivirus.

OX NCBI\_TaxID=11072;

RN [1]\_

RP SEQUENCE FROM N.A.

RC STRAIN=826309;

RA Cao J.X., Ni H., Sil B.K., Campbell G.A., Ryman K.D., Kitchen I., Barrett A.D.;

RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; U21054; AAA99710.1; -.

DR HSP; Q88653; IOKE.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR GO; GO:0019058; P:viral infectious cycle; IEA.

DR InterPro; IPR001122; Flavi\_capsidC.

DR InterPro; IPR000336; Flavi\_glycoprote.

DR InterPro; IPR000069; Flavi\_M.

DR InterPro; IPR002535; Flavi\_propep.

DR Pfam; PF01003; Flavi\_capsid; 1.

DR Pfam; PF00869; Flavi\_glycoprot; 1.

DR Pfam; PF02832; Flavi\_glycop\_C; 1.

DR Pfam; PF01004; Flavi\_M; 1.

DR Pfam; PF01570; Flavi\_propep; 1.

DR ProDom; PD001556; Flavi\_glycoprote; 1.

KW Envelope protein; Polyprotein.

FT CHAIN 1 127 core protein.

FT CHAIN 128 294 membrane protein.

FT CHAIN 295 >789 envelope protein.

FT NON\_TER 789 789

SQ SEQUENCE 789 AA; 85774 MW; 5B960E85754109A6 CRC64;

Query Match 75.4%; Score 89; DB 2; Length 789;

Best Local Similarity 100.0%; Pred. No. 0.0002;

```

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSIMMLASLAVVIACAGA 24
Db 110 GSIMMLASLAVVIACAGA 127

RESULT 8
Q86862 ID Q86862 PRELIMINARY; PRT; 793 AA.
AC Q86862;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Polyprotein (Fragment).
OS Japanese encephalitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=11072;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95066343; PubMed=7975862; DOI=10.1016/0264-410X(94)90294-1;
RA Hasegawa H., Yoshida M., Fujita S., Kobayashi Y.;
RT "Comparison of structural proteins among antigenically different
RT Japanese encephalitis virus strains."
RL Vaccine 12:841-844(1994).
DR EMBL; S75726; AAB32599.2; -.
DR PIR; B44055; B44055.
DR HSSP; Q88653; IOKE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0019058; F:viral infectious cycle; IEA.
DR InterPro; IPR001122; Flavi_capsidC.
DR InterPro; IPR000336; Flavi_glycoprote.
DR InterPro; IPR000069; Flavi_M.
DR InterPro; IPR002535; Flavi_propep.
DR Pfam; PF01003; Flavi_capsid; 1.
DR Pfam; PF00869; Flavi_glycoprot; 1.
DR Pfam; PF02832; Flavi_glycopC; 1.
DR Pfam; PF01004; Flavi_M; 1.
DR Pfam; PF01570; Flavi_propep; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
KW Polyprotein.
FT NON_TER 1
FT NON_TER 793
SQ SEQUENCE 793 AA; 86179 MW; 306934673DC005E5 CRC64;

Query Match 75.4%; Score 89; DB 2; Length 793;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSIMMLASLAVVIACAGA 24
Db 109 GSIMMLASLAVVIACAGA 126

RESULT 9
Q82869 ID Q82869 PRELIMINARY; PRT; 794 AA.
AC Q82869;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Polyprotein (Fragment).
OS Japanese encephalitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=11072;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SA14-5-3;
RX MEDLINE=94267439; PubMed=8207417;

Query Match 75.4%; Score 89; DB 2; Length 793;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSIMMLASLAVVIACAGA 24
Db 110 GSIMMLASLAVVIACAGA 127

RESULT 10
Q82870 ID Q82870 PRELIMINARY; PRT; 794 AA.
AC Q82870;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Polyprotein (Fragment).
OS Japanese encephalitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=11072;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SA14;
RX MEDLINE=94267439; PubMed=8207417;
RA Ni H., Burns N.J., Chang G.J., Zhang M.J., Wills M.R., Trent D.W.,
RA Sanders P.G., Barrett A.D.;
RT "Comparison of nucleotide and deduced amino acid sequence of the 5'
RT non-coding region and structural protein genes of the wild-type
RT Japanese encephalitis virus strain SA14 and its attenuated vaccine
RT derivatives."
RL J. Gen. Virol. 75:1505-1510(1994).
DR EMBL; U04521; AAA67173.1; -.
DR PIR; B44055; B44055.
DR HSSP; Q88653; IOKE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0019058; F:viral infectious cycle; IEA.
DR InterPro; IPR001122; Flavi_capsidC.
DR InterPro; IPR000336; Flavi_glycoprote.
DR InterPro; IPR000069; Flavi_M.
DR InterPro; IPR002535; Flavi_propep.
DR Pfam; PF01003; Flavi_capsid; 1.
DR Pfam; PF00869; Flavi_glycoprot; 1.
DR Pfam; PF02832; Flavi_glycopC; 1.
DR Pfam; PF01004; Flavi_M; 1.
DR Pfam; PF01570; Flavi_propep; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
KW Polyprotein.
FT CHAIN 1 127 C.
FT CHAIN 128 294 prM/M.
FT CHAIN 295 >794 E.
FT NON_TER 794
SQ SEQUENCE 794 AA; 86318 MW; 5E4400E2011C3581 CRC64;

Query Match 75.4%; Score 89; DB 2; Length 794;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSIMMLASLAVVIACAGA 24
Db 110 GSIMMLASLAVVIACAGA 127

RESULT 11
Q82870 ID Q82870 PRELIMINARY; PRT; 794 AA.
AC Q82870;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Polyprotein (Fragment).
OS Japanese encephalitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=11072;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SA14;
RX MEDLINE=94267439; PubMed=8207417;
RA Ni H., Burns N.J., Chang G.J., Zhang M.J., Wills M.R., Trent D.W.,
RA Sanders P.G., Barrett A.D.;
RT "Comparison of nucleotide and deduced amino acid sequence of the 5'
RT non-coding region and structural protein genes of the wild-type
RT Japanese encephalitis virus strain SA14 and its attenuated vaccine
RT derivatives."
RL J. Gen. Virol. 75:1505-1510(1994).
DR EMBL; U04522; AAA67174.1; -.
DR PIR; B44055; B44055.
DR HSSP; Q88653; IOKE.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0019058; F:viral infectious cycle; IEA.
DR InterPro; IPR001122; Flavi_capsidC.
DR InterPro; IPR000336; Flavi_glycoprote.
DR InterPro; IPR000069; Flavi_M.

```

DR InterPro; IPR002535; Flavi\_propep.  
 DR Pfam; PF01003; Flavi\_capsid; 1.  
 DR Pfam; PF00869; Flavi\_glycoprot; 1.  
 DR Pfam; PF02832; Flavi\_glycop\_C; 1.  
 DR Pfam; PF01004; Flavi\_M; 1.  
 DR Pfam; PF01570; Flavi\_propep; 1.  
 DR ProDom; PD001556; Flavi\_glycoproteE; 1.  
 KW Polyprotein.  
 FT CHAIN 1 127 C.  
 FT CHAIN 128 294 prM/M.  
 FT CHAIN 295 >794 E.  
 FT NON\_TER 794  
 SQ SEQUENCE 794 AA; 86141 MW; 5D45F78B9EBEB885 CRC64;

Query Match 75.4%; Score 89; DB 2; Length 794;  
 Best Local Similarity 100.0%; Pred. No. 0.0002;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSIMMLASLAVVIACAGA 24  
 |||||  
 Db 110 GSIMMLASLAVVIACAGA 127

## RESULT 11

Q98WK2 PRELIMINARY; PRT; 1437 AA.  
 AC Q98WK2;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Structural protein (Fragment).  
 OS Japanese encephalitis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Flavivirus.  
 OX NCBI\_TaxID=11072;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Liu J.-J.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY027863; AAK15789.1; -.  
 DR FIR; B44055; B44055.  
 DR HSP; Q88653; LOXE.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR GO; GO:0019058; P:viral infectious cycle; IEA.  
 DR InterPro; IPR001122; Flavi\_capsidC.  
 DR InterPro; IPR000336; Flavi\_glycoproteE.  
 DR InterPro; IPR000069; Flavi\_M.  
 DR InterPro; IPR001157; Flavi\_NS1.  
 DR InterPro; IPR000752; Flavi\_NS2A.  
 DR InterPro; IPR000487; Flavi\_propep.  
 DR InterPro; IPR002535; Flavi\_propep.  
 DR Pfam; PF01003; Flavi\_capsid; 1.  
 DR Pfam; PF00869; Flavi\_glycoprot; 1.  
 DR Pfam; PF02832; Flavi\_glycop\_C; 1.  
 DR Pfam; PF01004; Flavi\_M; 1.  
 DR Pfam; PF00948; Flavi\_NS1; 1.  
 DR Pfam; PF01005; Flavi\_NS2A; 1.  
 DR Pfam; PF01002; Flavi\_NS2B; 1.  
 DR Pfam; PF01570; Flavi\_propep; 1.  
 DR ProDom; PD001556; Flavi\_glycoproteE; 1.  
 DR ProDom; PD001496; Flavi\_NS1; 1.  
 FT NON\_TER 1437 1437  
 SQ SEQUENCE 1437 AA; 157823 MW; B0F6227AD2346BFF CRC64;

Query Match 75.4%; Score 89; DB 2; Length 1437;  
 Best Local Similarity 100.0%; Pred. No. 0.00032;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSIMMLASLAVVIACAGA 24  
 |||||  
 Db 110 GSIMMLASLAVVIACAGA 127

## RESULT 12

POLG\_JAEVN STANDARD; PRT; 1440 AA.  
 ID POLG\_JAEVN  
 AC P14403; P08769;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Genome polyprotein [Contains: Capsid protein C (Core protein); Matrix protein (Envelope glycoprotein M); Major envelope protein E; Nonstructural protein NS1; Nonstructural protein NS2A; Flavivirin (EC 3.4.21.91) (NS2B/NS3 proteinase)] (Fragment).  
 OS Japanese encephalitis virus (strain Nakayama).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Flavivirus.  
 OX NCBI\_TaxID=11076;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87236200; PubMed=3035787;  
 RA McAda P.C.; Mason P.W.; Schmaljohn C.S.; Dalrymple J.M.; Mason T.L.; Fournier M.J.;  
 RA "partial nucleotide sequence of the Japanese encephalitis virus genome.";  
 RL Virology 158:348-360(1987).  
 CC -!- FUNCTION: The small proteins NS2A, NS4A and NS4B are hydrophobic, suggesting a possible membrane-related function. NS5 may play a role in the viral RNA replication. NS3 and NS2B form a protease which processes the viral polyprotein into separate proteins.  
 CC -!- CATALYTIC ACTIVITY: Selective hydrolysis of Xaa-Xaa-Xbb bonds in which each of the Xaa can be either Arg or Lys and Xbb can be either Ser or Ala.  
 CC -!- SUBUNIT: The virion of this virus is a nucleocapsid covered by a lipoprotein envelope. The envelope consists of two proteins: protein M and glycoprotein E. The nucleocapsid is a complex of protein C and mRNA. In immature particles, there are 60 icosahedrally organized trimeric spikes on the surface. Each spike consists of three heterodimers of envelope protein M precursor (prM) and envelope protein E (By similarity).  
 CC

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EMBL; M16574; AAA46251.1; -.  
 FIR; A27844; GNMVJF.  
 DR HSP; Q88653; LOXE.  
 DR InterPro; IPR001122; Flavi\_capsidC.  
 DR InterPro; IPR000336; Flavi\_glycoproteE.  
 DR InterPro; IPR000069; Flavi\_M.  
 DR InterPro; IPR001157; Flavi\_NS1.  
 DR InterPro; IPR000752; Flavi\_NS2A.  
 DR InterPro; IPR000487; Flavi\_propep.  
 DR InterPro; IPR002535; Flavi\_propep.  
 DR Pfam; PF01003; Flavi\_capsid; 1.  
 DR Pfam; PF02832; Flavi\_glycop\_C; 1.  
 DR Pfam; PF00869; Flavi\_glycoprot; 1.  
 DR Pfam; PF01004; Flavi\_M; 1.  
 DR Pfam; PF00948; Flavi\_NS1; 1.  
 DR Pfam; PF01005; Flavi\_NS2A; 1.  
 DR Pfam; PF01002; Flavi\_NS2B; 1.  
 DR Pfam; PF01570; Flavi\_propep; 1.  
 DR ProDom; PD001556; Flavi\_glycoproteE; 1.  
 DR ProDom; PD001496; Flavi\_NS1; 1.  
 KW ATP-binding; Coat protein; Core protein; Envelope protein; Polyprotein;  
 KW Glycoprotein; Helicase; Hydrolase; Nonstructural protein; Polyprotein;  
 KW Transmembrane.  
 FT NON\_TER 1 1  
 FT CHAIN <1 53 Capsid protein C.

FT PROPEP 54 146 Envelope glycoprotein M.  
 FT CHAIN 147 222 Major envelope protein E.  
 FT CHAIN 223 794 Nonstructural protein NS1.  
 FT CHAIN 795 1136 Nonstructural protein NS2A.  
 FT CHAIN 1137 1301 Flavivirin protease subunit NS2B.  
 FT CHAIN 1302 1432 Flavivirin protease subunit NS3.  
 FT CHAIN 1433 >1440 By similarity.  
 FT DISULFID 282 252 By similarity.  
 FT DISULFID 285 338 By similarity.  
 FT DISULFID 296 327 By similarity.  
 FT DISULFID 314 343 By similarity.  
 FT DISULFID 412 509 By similarity.  
 FT DISULFID 526 557 By similarity.  
 FT CARBOHYD 68 68 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 376 376 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 852 852 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 929 929 N-linked (GlcNAc...) (Potential).  
 FT NON\_TER 1440 1440  
 SQ SEQUENCE 1440 AA; 158184 MW; 4D489A365A3C2E6E CRC64;

Query Match 75.4%; Score 89; DB 1; Length 1440;  
 Best Local Similarity 100.0%; Pred. No. 0.00032;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSIMMLASLAVVIACAGA 24  
 Db 36 GSIMMLASLAVVIACAGA 53

## RESULT 13

Q04092  
 ID Q04092 PRELIMINARY; PRT; 1504 AA.  
 AC Q04092;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Polyprotein (Fragment).  
 OS Japanese encephalitis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Flavivirus.  
 OC NCBI\_TaxID=11072;  
 RN [1]  
 RA Konishi E., Pincus S., Fonseca B.A.L., Shope R.E., Paoletti E.,  
 RA Mason P.W.,  
 RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; M73710; AAA46250.1; -;  
 DR PIR; B44055; B44055.  
 DR HSP; Q88653; 10KE.  
 DR GO; GO:0013028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR GO; GO:0013058; F:viral infectious cycle; IEA.  
 DR InterPro; IPR001122; Flavi\_capsidC.  
 DR InterPro; IPR000336; Flavi\_glycoprote.  
 DR InterPro; IPR000089; Flavi\_M.  
 DR InterPro; IPR001157; Flavi\_NS1.  
 DR InterPro; IPR000752; Flavi\_NS2A.  
 DR InterPro; IPR000487; Flavi\_NS2B.  
 DR InterPro; IPR002535; Flavi\_propep.  
 DR Pfam; PF01003; Flavi\_capsid; 1.  
 DR Pfam; PF00869; Flavi\_glycoprote; 1.  
 DR Pfam; PF02832; Flavi\_glycop\_C; 1.  
 DR Pfam; PF01004; Flavi\_M; 1.  
 DR Pfam; PF00948; Flavi\_NS1; 1.  
 DR Pfam; PF01005; Flavi\_NS2A; 1.  
 DR Pfam; PF01002; Flavi\_NS2B; 1.  
 DR Pfam; PF01570; Flavi\_propep; 1.  
 DR ProDom; PD001556; Flavi\_glycoprote; 1.  
 DR ProDom; PD001496; Flavi\_NS1; 1.  
 DR NON\_TER 1 1  
 FT CHAIN 2 105 capsid protein.

FT CHAIN 795 1146 nonstructural protein 2.  
 FT CHAIN 1147 1373 nonstructural protein 2A.  
 FT CHAIN 1374 1504 nonstructural protein 2B.  
 FT CHAIN 128 294 membrane protein precursor.  
 FT CHAIN 220 294 membrane protein.  
 FT CHAIN 235 794 envelope protein.  
 SQ SEQUENCE 1504 AA; 165069 MW; 101EB822FCD1601 CRC64;

Query Match 75.4%; Score 89; DB 2; Length 1504;  
 Best Local Similarity 100.0%; Pred. No. 0.00033;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSIMMLASLAVVIACAGA 24  
 Db 110 GSIMMLASLAVVIACAGA 127

## RESULT 14

POLG\_JAEV1  
 ID POLG\_JAEV1 STANDARD; PRT; 3432 AA.  
 AC P27395; Q82920; Q82921; Q82922; Q82923; Q82924; Q82925; Q82926;  
 AC Q82927; Q82928;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Genome polyprotein [Contains: Capsid protein C (Core protein); Matrix  
 protein (Envelope protein M); Major envelope protein E; Nonstructural  
 proteins NS1, NS2A, NS4A and NS4B; Flavivirin (EC 3.4.21.91) (NS2B/NS3  
 proteinase); RNA-directed RNA polymerase (EC 2.7.7.48) (NS5)].  
 OS Japanese encephalitis virus (strain SA-14).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Flavivirus.  
 OC NCBI\_TaxID=11073;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90320126; PubMed=2371768;  
 RA Nitayaphan S., Grant J.A., Chang G.J.J., Trent D.W.;  
 RT "Nucleotide sequence of the virulent SA-14 strain of Japanese  
 encephalitis virus and its attenuated vaccine derivative, SA-14-14-  
 2";  
 RL Virology 177:541-552(1990).  
 CC -!- FUNCTION: The small proteins NS2A, NS4A and NS4B are hydrophobic,  
 suggesting a possible membrane-related function. NS5 may play a  
 role in the viral RNA replication. NS3 and NS2B form a protease  
 which processes the viral polyprotein into separate proteins.  
 CC -!- CATALYTIC ACTIVITY: Selective hydrolysis of Xaa-Xaa|-Xbb bonds in  
 which each of the Xaa can be either Arg or Lys and Xbb can be  
 either Ser or Ala.  
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
 {RNA}(N).  
 CC -!- SUBUNIT: The virion of this virus is a nucleocapsid covered by a  
 lipoprotein envelope. The envelope consists of two proteins:  
 protein M and glycoprotein E. The nucleocapsid is a complex of  
 protein C and mRNA. In immature particles, there are 60  
 icosadially organized trimeric spikes on the surface. Each spike  
 consists of three heterodimers of envelope protein M precursor  
 (pM) and envelope protein E (by similarity).  
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration  
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 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL; M55506; AAA46248.1; -;  
 DR EMBL; M55506; AAA46249.1; ALT\_INIT.  
 DR InterPro; IPR001410; DEAD.  
 DR InterPro; IPR002464; DEAD\_box.  
 DR InterPro; IPR001122; Flavi\_capsidC.  
 DR InterPro; IPR000336; Flavi\_glycoprote.  
 DR InterPro; IPR000069; Flavi\_M.



DR InterPro; IPR001157; Flavi\_Ns1.  
 DR InterPro; IPR000752; Flavi\_NS2A.  
 DR InterPro; IPR000487; Flavi\_NS2B.  
 DR InterPro; IPR000404; Flavi\_NS4A.  
 DR InterPro; IPR001528; Flavi\_NS4B.  
 DR InterPro; IPR000208; Flavi\_NS5.  
 DR InterPro; IPR002535; Flavi\_propep.  
 DR InterPro; IPR001650; Helicase\_C.  
 DR InterPro; IPR001850; Peptidase\_S7.  
 DR InterPro; IPR007095; RNA\_pol\_DS\_PS.  
 DR InterPro; IPR007094; RNA\_pol\_PSVir.  
 DR InterPro; IPR002877; RrmJFtsJ\_mfrase.  
 DR Pfam; PF01003; Flavi\_capsid; 1.  
 DR Pfam; PF00869; Flavi\_glycoprot; 1.  
 DR Pfam; PF02832; Flavi\_glycoprot; 1.  
 DR Pfam; PF01004; Flavi\_M; 1.  
 DR Pfam; PF00948; Flavi\_Ns1; 1.  
 DR Pfam; PF01005; Flavi\_NS2A; 1.  
 DR Pfam; PF01002; Flavi\_NS2B; 1.  
 DR Pfam; PF01350; Flavi\_NS4A; 1.  
 DR Pfam; PF01349; Flavi\_NS4B; 1.  
 DR Pfam; PF00972; Flavi\_NS5; 1.  
 DR Pfam; PF01570; Flavi\_propep; 1.  
 DR Pfam; PF01728; FtsJ; 1.  
 DR Pfam; PF00271; Helicase\_C; 1.  
 DR Pfam; PF00949; Peptidase\_S7; 1.  
 DR ProDom; PD001556; Flavi\_glycoprotB; 1.  
 DR ProDom; PD001496; Flavi\_Ns1; 1.  
 DR PROSITE; PS00690; DEAH\_ATP\_HELICASE; FALSE NEG.  
 KW ATP-binding; Coat protein; Core protein; Envelope protein;  
 KW Glycoprotein; Helicase; Hydroxylase; Nonstructural protein; Polypeptide;  
 KW RNA-directed RNA polymerase; Transference; Transmembrane.  
 FT INIT\_MET 1  
 FT CHAIN 1 127  
 FT PROPEP 128 219  
 FT CHAIN 220 294  
 FT CHAIN 295 794  
 FT CHAIN 795 1206  
 FT CHAIN 1207 1373  
 FT CHAIN 1374 1504  
 FT CHAIN 1505 2123  
 FT CHAIN 2124 2412  
 FT CHAIN 2413 2527  
 FT CHAIN 2528 3432  
 FT CHAIN 3432 1705  
 FT NP\_BIND 1698 1705  
 FT ACT\_SITE 1555 1555  
 FT ACT\_SITE 1579 1579  
 FT ACT\_SITE 1639 1639  
 FT SITE 1789 1792  
 FT TRANSMEM 44 60  
 FT TRANSMEM 112 127  
 FT TRANSMEM 280 294  
 FT TRANSMEM 774 790  
 FT DISULFID 297 324  
 FT DISULFID 354 410  
 FT DISULFID 368 399  
 FT DISULFID 386 415  
 FT DISULFID 484 581  
 FT DISULFID 598 629  
 FT CARBOHYD 142 142  
 FT CARBOHYD 448 448  
 FT CARBOHYD 924 924  
 FT CARBOHYD 1001 1001  
 FT CARBOHYD 1594 1594  
 FT CARBOHYD 2463 2463  
 FT CARBOHYD 2491 2491  
 FT CARBOHYD 2761 2761  
 FT CARBOHYD 2866 2866  
 FT CARBOHYD 2904 2904  
 SQ SEQUENCE 3432 AA; 380205 MW; 11B9423735B1B3FE CRC64;

Query Match

75.4%; Score 89; DB 1; Length 3432;

Best Local Similarity 100.0%; Pred. No. 0.00065;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 GSIMWLASLAVVIACAGA 24  
 DB 110 GSIMWLASLAVVIACAGA 127  
 RESULT 15  
 POLG\_JAEV5  
 ID POLG\_JAEV5 STANDARD; PRT; 3432 AA.  
 AC P19110;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Genome polyprotein [Contains: Capsid protein C (Core protein); Matrix  
 DE protein (Envelope protein M); Major envelope protein E; Nonstructural  
 DE proteins NS1, NS2A, NS4A and NS4B; Flavivirin (EC 3.4.21.91) (NS2B/NS3  
 DE proteinase); RNA-directed RNA polymerase (EC 2.7.7.48) (NS5)].  
 OS Japanese encephalitis virus (strain SA(v)).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Flavivirus.  
 OX NCBI\_TaxID=11074;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91280801; PubMed=1829286;  
 RA Aihara S., Rao C., Yu Y.X., Lee T., Watanabe K., Komiya T.,  
 RA Sumiyoshi H., Hashimoto H., Nomoto A.;  
 RT "Identification of mutations that occurred on the genome of Japanese  
 RT encephalitis virus during the attenuation process.";  
 RL Virus Genes 5:95-109(1991).  
 CC -!- FUNCTION: The small proteins NS2A, NS4A and NS4B are hydrophobic,  
 CC suggesting a possible membrane-related function. NS5 may play a  
 CC role in the viral RNA replication. NS3 and NS2B form a protease  
 CC which processes the viral polyprotein into separate proteins.  
 CC -!- CATALYTIC ACTIVITY: Selective hydrolysis of Xaa-Xaa-|-Xbb bonds in  
 CC which each of the Xaa can be either Arg or Lys and Xbb can be  
 CC either Ser or Ala.  
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
 CC (RNA)(N).  
 CC -!- SUBUNIT: The virion of this virus is a nucleocapsid covered by a  
 CC lipoprotein envelope. The envelope consists of two proteins:  
 CC protein M and glycoprotein E. The nucleocapsid is a complex of  
 CC protein C and mRNA. In immature particles, there are 60  
 CC icosadially organized trimeric spikes on the surface. Each spike  
 CC consists of three heterodimers of envelope protein M precursor  
 CC (pM) and envelope protein E (By similarity).  
 CC -!- SIMILARITY: Contains 1 peptidase S7 domain.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; D90194; BAA14218.1; -.  
 CC HSSP; Q88653; IL9K.  
 CC MEROPS; S07.001; -.  
 CC InterPro; IPR001410; DEAD.  
 CC InterPro; IPR002464; DEAH\_box.  
 CC InterPro; IPR001122; Flavi\_capsidC.  
 CC InterPro; IPR000336; Flavi\_glycoprote.  
 CC InterPro; IPR000069; Flavi\_M.  
 CC InterPro; IPR001157; Flavi\_Ns1.  
 CC InterPro; IPR000752; Flavi\_NS2A.  
 CC InterPro; IPR000487; Flavi\_NS2B.  
 CC InterPro; IPR000404; Flavi\_NS4A.  
 CC InterPro; IPR001528; Flavi\_NS4B.  
 CC InterPro; IPR000208; Flavi\_NS5.  
 CC InterPro; IPR002535; Flavi\_propep.  
 CC InterPro; IPR001650; Helicase\_C.

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DR InterPro; IPR001850; Peptidase S7.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSvir.
DR InterPro; IPR002877; RrmJftsJ_mtfase.
DR Pfam; PF01003; Flavi_Capsid; 1.
DR Pfam; PF00869; Flavi_Glycoprot; 1.
DR Pfam; PF02832; Flavi_Glycop_C; 1.
DR Pfam; PF01004; Flavi_M; 1.
DR Pfam; PF00948; Flavi_NSI; 1.
DR Pfam; PF01005; Flavi_NS2A; 1.
DR Pfam; PF01002; Flavi_NS2B; 1.
DR Pfam; PF01350; Flavi_NS4A; 1.
DR Pfam; PF01349; Flavi_NS4B; 1.
DR Pfam; PF00972; Flavi_NS5; 1.
DR Pfam; PF01570; Flavi_propep; 1.
DR Pfam; PF01728; FtsJ; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF00949; Peptidase S7; 1.
DR ProDom; PD001556; Flavi_Glycoprote; 1.
DR ProDom; PD001496; Flavi_NSI; 1.
DR PROSITE; PS00890; DEAH_Atp_HELICASE; FALSE NEG.
KW ATP-binding; Coat protein; Core protein; Envelope protein;
KW Glycoprotein; Helicase; Hydrolase; Nonstructural protein; Polyprotein;
KW RNA-directed RNA polymerase; Transferase; Transmembrane.
FT INIT_MET 1 1
FT CHAIN 1 127
FT PROPEP 128 219
FT CHAIN 220 294
FT CHAIN 295 794
FT CHAIN 795 1206
FT CHAIN 1207 1373
FT CHAIN 1374 1504
FT CHAIN 1505 2123
FT CHAIN 2124 2412
FT CHAIN 2413 2527
FT CHAIN 2528 3432
FT NP_BIND 1698 1705
FT ACT_SITE 1555 1555
FT ACT_SITE 1579 1579
FT ACT_SITE 1639 1639
FT SITE 1789 1792
FT TRANSMEM 44 60
FT TRANSMEM 112 127
FT TRANSMEM 280 284
FT TRANSMEM 774 790
FT DISULFID 237 324
FT DISULFID 354 410
FT DISULFID 368 399
FT DISULFID 386 415
FT DISULFID 484 581
FT DISULFID 598 629
FT CARBOHYD 142 142
FT CARBOHYD 448 448
FT CARBOHYD 924 924
FT CARBOHYD 1001 1001
FT CARBOHYD 2463 2463
FT CARBOHYD 2491 2491
FT SEQUENCE 3432 AA; 380176 MW; AE8A63E0C00C4674 CRC64;
Query Match 75.4%; Score 89; DB 1; Length 3432;
Best Local Similarity 100.0%; Pred.No.0.00065;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GSIMWLASLAVVIACAGA 24
Db 110 GSIMWLASLAVVIACAGA 127
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Search completed: October 26, 2005, 01:34:30  
Job time : 171 secs



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Query Match      66.1%; Score 78; DB 6; Length 970;
Best Local Similarity 94.4%; Pred. No. 0.0016; 1; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GSIMMLASLAVVIACAGA 24
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Db 60 GSIMMLASLAVVIAYAGA 77

RESULT 3
US-09-711-164-393
; Patent No. 5229293
; APPLICANT: MATSUURA, YOSHIHARU-YASUI, KOTARO,SATO, TAKANORI
; TITLE OF INVENTION: RECOMBINANT BACULOVIRUS
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; FILING DATE: 05-MAY-1989
; SEQ ID NO:2:
; LENGTH: 970
5229293-2

Query Match      66.1%; Score 78; DB 6; Length 970;
Best Local Similarity 94.4%; Pred. No. 0.0016; 1; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GSIMMLASLAVVIACAGA 24
   |||||
Db 60 GSIMMLASLAVVIAYAGA 77

RESULT 4
US-09-711-164-393
; Sequence 393, Application US/09711164
; Patent No. 6589738
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERET
; FILE REFERENCE: ELITRA.008A
; CURRENT APPLICATION NUMBER: US/09/711,164
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/164415
; PRIOR FILING DATE: 1999-11-9
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 393
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-711-164-393

Query Match      42.4%; Score 50; DB 4; Length 385;
Best Local Similarity 37.5%; Pred. No. 11;
Matches 9; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 MCKRSAGSIMMLASLAVVIACAGA 24
   : : |||
Db 103 LARTSLGSGFWLAAALALACSDA 126

RESULT 5
US-09-328-352-7069
; Sequence 7069, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
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; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7069
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7069

Query Match      42.4%; Score 50; DB 4; Length 443;
Best Local Similarity 42.1%; Pred. No. 13;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 5 SAGSIMMLASLAVVIACAG 23
   |||
Db 175 SDGNLLWISITVVAIACIG 193

RESULT 6
US-09-489-039A-13709
; Sequence 13709, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13709
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13709

Query Match      40.7%; Score 48; DB 4; Length 493;
Best Local Similarity 50.0%; Pred. No. 30;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 9 IMWLASLAVVIACAGA 24
   : |||||
Db 133 LVWLASLSLLVAFVGA 148

RESULT 7
US-09-543-681A-6077
; Sequence 6077, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6077
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6077

Query Match      40.7%; Score 48; DB 4; Length 510;
Best Local Similarity 56.2%; Pred. No. 31;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 9 IMWLASLAVVIACAGA 24
   : |||||
Db 111 LMWLASLAVIVAFCSA 126
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RESULT 8
US-09-815-923-4
; Sequence 4, Application US/09815923
; Patent No. 6787642
; GENERAL INFORMATION:
; APPLICANT: Gill, Sarjeet S.
; APPLICANT: Ross, Linda S.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Use of Insect Cell Membrane Transporters as No. 6787642el
; TITLE OF INVENTION: target Sites for Insecticides
; FILE REFERENCE: 023070-093800US
; CURRENT APPLICATION NUMBER: US/09/815,923
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 587
; TYPE: PRT
; ORGANISM: Manduca sexta
; FEATURE:
; OTHER INFORMATION: serotonin transporter
US-09-815-923-4

Query Match 40.7%; Score 48; DB 4; Length 587;
Best Local Similarity 53.3%; Pred. No. 36;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 GKRSAGSIMWLASLA 16
DB 232 GVSAGKVVWVWALA 246

RESULT 9
US-08-905-223-344
; Sequence 344, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 344:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; ORIGINAL SOURCE:

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; ORGANISM: Homo Sapiens
; TISSUE TYPE: Brain
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -23...-1
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 4.8
; OTHER INFORMATION: seq VNWVLALLEMCVC/KK
US-08-905-223-344

Query Match 39.0%; Score 46; DB 3; Length 27;
Best Local Similarity 38.9%; Pred. No. 2.3;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 RSAGSIMWLASLAVVIAC 21
DB 6 KTKGSVWVWVLALLEMCVC 23

RESULT 10
US-09-602-787A-420
; Sequence 420, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Krüger, Burkhard
; APPLICANT: Schöder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/09/602,787A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932190.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932191.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932228.7
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932229.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932927.3
; PRIOR FILING DATE: 1999-07-14

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; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940765.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940766.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940830.0
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940831.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940832.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940833.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941395.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942077.7
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942078.5
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942079.3
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 420
; TYPE: PRT
; LENGTH: 129
; ORGANISM: Corynebacterium glutamicum
US-09-602-787A-420

Query Match 39.0%; Score 46; DB 4; Length 129;
Best Local Similarity 36.4%; Pred. No. 13;
Matches 8; Conservative 7; Mismatches 7; Indels 7; Gaps 0;

QY 1 MGKRSAGSIMMLASLAVVIACA 22
Db 37 IGLRIFGAVLWAASISSVIGAS 58

RESULT 11
US-08-440-856A-3
; Sequence 3, Application US/08440856A
; Patent No. 5750873
; GENERAL INFORMATION:
; APPLICANT: DELLAPORTA, STEPHEN L.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
; TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 2000 PENNSYLVANIA AVE. N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,856A
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A.
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 05463-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1517
; TELEFAX: (202) 887-0763
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-440-856A-3

Query Match 39.0%; Score 46; DB 1; Length 337;
Best Local Similarity 47.8%; Pred. No. 39;
Matches 11; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGKRSAGSIMMLASLAVVIACAG 23
Db 181 MAPRRAGSIVSVASVAAVLGGIG 203

RESULT 12
US-09-602-787A-418
; Sequence 418, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Kr'ger, Burkhard
; APPLICANT: Sch'der, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/09/602,787A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932190.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932191.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932228.7
; PRIOR FILING DATE: 1999-07-09

;; PRIOR APPLICATION NUMBER: DE 19932229.5  
;; PRIOR FILING DATE: 1999-07-09  
;; PRIOR APPLICATION NUMBER: DE 19932230.9  
;; PRIOR FILING DATE: 1999-07-09  
;; PRIOR APPLICATION NUMBER: DE 19932927.3  
;; PRIOR FILING DATE: 1999-07-14  
;; PRIOR APPLICATION NUMBER: DE 19933005.0  
;; PRIOR FILING DATE: 1999-07-14  
;; PRIOR APPLICATION NUMBER: DE 19933006.9  
;; PRIOR FILING DATE: 1999-07-14  
;; PRIOR APPLICATION NUMBER: DE 19940764.9  
;; PRIOR FILING DATE: 1999-08-27  
;; PRIOR APPLICATION NUMBER: DE 19940765.7  
;; PRIOR FILING DATE: 1999-08-27  
;; PRIOR APPLICATION NUMBER: DE 19940766.5  
;; PRIOR FILING DATE: 1999-08-27  
;; PRIOR APPLICATION NUMBER: DE 19940830.0  
;; PRIOR FILING DATE: 1999-08-27  
;; PRIOR APPLICATION NUMBER: DE 19940831.9  
;; PRIOR FILING DATE: 1999-08-27  
;; PRIOR APPLICATION NUMBER: DE 19940832.7  
;; PRIOR FILING DATE: 1999-08-27  
;; PRIOR APPLICATION NUMBER: DE 19940833.5  
;; PRIOR FILING DATE: 1999-08-27  
;; PRIOR APPLICATION NUMBER: DE 19941378.9  
;; PRIOR FILING DATE: 1999-08-31  
;; PRIOR APPLICATION NUMBER: DE 19941379.7  
;; PRIOR FILING DATE: 1999-08-31  
;; PRIOR APPLICATION NUMBER: DE 19941395.9  
;; PRIOR FILING DATE: 1999-08-31  
;; PRIOR APPLICATION NUMBER: DE 19942077.7  
;; PRIOR FILING DATE: 1999-09-03  
;; PRIOR APPLICATION NUMBER: DE 19942078.5  
;; PRIOR FILING DATE: 1999-09-03  
;; PRIOR APPLICATION NUMBER: DE 19942079.3  
;; PRIOR FILING DATE: 1999-09-03  
;; PRIOR APPLICATION NUMBER: DE 19942088.2  
;; PRIOR FILING DATE: 1999-09-03  
;; NUMBER OF SEQ ID NOS: 678  
;; SEQ ID NO 418  
;; LENGTH: 396  
;; TYPE: PRT  
;; ORGANISM: Corynebacterium glutamicum  
US-09-602-787A-418

Query Match 39.0%; Score 46; DB 4; Length 396;  
Best Local Similarity 36.4%; Pred. No. 47;  
Matches 8; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 MGKRSAGSIMMLASLAVVIACA 22  
DB 304 IGLRIFGAVLWASISSVIGAS 325

RESULT 13  
US-09-489-039A-10428  
; Sequence 10428, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Berton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709-2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 10428  
; LENGTH: 414  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-10428

Query Match 39.0%; Score 46; DB 4; Length 414;  
Best Local Similarity 30.0%; Pred. No. 49;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 WLASLAVVIA 20  
DB 171 WLASLAVIA 180

RESULT 14  
US-08-817-441-46  
; Sequence 46, Application US/08817441  
; Patent No. 6399294  
; GENERAL INFORMATION:  
; APPLICANT: CHARNEAU, PIERRE  
; APPLICANT: CLAVEL, FRANCOISE  
; APPLICANT: BORMAN, ANDREW  
; APPLICANT: QUILLIENT, CAROLINE  
; APPLICANT: GUETARD, DENISE  
; APPLICANT: MONTAGNIER, LUC  
; APPLICANT: DONJON DE SAINT-MARTIN, JACQUELINE  
; APPLICANT: COHEN, JACQUES  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner, L.L.P.  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/817,441  
; FILING DATE: 11-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR 95/01391  
; FILING DATE: 20-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 9412554  
; FILING DATE: 20-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 9502526  
; FILING DATE: 03-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 03260.6005-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 526 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-817-441-46

Query Match 38.1%; Score 45; DB 3; Length 526;  
Best Local Similarity 42.9%; Pred. No. 92;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGKRSAGSIMMLASLAVVIAC 21  
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Db 8 MGKRNKLGWCLILALIIPC 28

RESULT 15

US-08-817-441-102  
; Sequence 102, Application US/08817441  
; Patent No. 6399294  
; GENERAL INFORMATION:  
; APPLICANT: CHARNEAU, PIERRE  
; APPLICANT: CLAVEL, FRANCOISE  
; APPLICANT: BORMAN, ANDREW  
; APPLICANT: QUILLIENT, CAROLINE  
; APPLICANT: GUETARD, DENISE  
; APPLICANT: MONTAGNIER, LUC  
; APPLICANT: DONJON DE SAINT-MARTIN, JACQUELINE  
; APPLICANT: COHEN, JACQUES  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR  
; TITLE OF INVENTION: SUBTYPE) ANTIGENS  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner, L.L.P.  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/817,441  
; FILING DATE: 11-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR 95/01391  
; FILING DATE: 20-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 9412554  
; FILING DATE: 20-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 9502526  
; FILING DATE: 03-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 03260.6005-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 102:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 877 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-817-441-102

Query Match 38.1%; Score 45; DB 3; Length 877;  
Best Local Similarity 42.9%; Pred. No. 1.6e+02;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Oy 1 MGKRSAGSIMWLASLAVIAC 21  
Db 8 MGKRNKLGWCLILALIIPC 28

Search completed: October 26, 2005, 01:36:01  
Job time : 43 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 26, 2005, 01:34:40 ; Search time 163 Seconds  
(without alignments)  
61.474 Million cell updates/sec

Title: US-09-826-115A-14

Perfect score: 118

Sequence: 1 MGKRSAGSIMVLASLAVVIACAGA 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
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6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US10F\_PUBCOMB.pep:\*  
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22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	118	100.0	24	18	US-10-500-796A-14
3	118	100.0	33	18	US-10-500-796A-37
4	118	100.0	685	18	US-10-500-796A-43
5	118	100.0	685	18	US-10-500-796A-45
6	118	100.0	685	18	US-10-500-796A-47
7	118	100.0	692	10	US-09-826-115-16
8	118	100.0	692	18	US-10-500-796A-16
9	96	81.4	24	10	US-09-826-115-27
10	96	81.4	24	18	US-10-500-796A-27
11	96	81.4	681	10	US-09-826-115-20

12	96	81.4	681	10	US-09-826-115-24	Sequence 24, Appl
13	96	81.4	681	18	US-10-500-796A-24	Sequence 24, Appl
14	96	81.4	685	18	US-10-500-796A-20	Sequence 20, Appl
15	96	81.4	692	10	US-09-826-115-22	Sequence 22, Appl
16	96	81.4	692	18	US-10-500-796A-22	Sequence 22, Appl
17	91	77.1	39	18	US-10-500-796A-35	Sequence 35, Appl
18	91	77.1	697	10	US-09-826-115-11	Sequence 11, Appl
19	91	77.1	697	10	US-09-826-115-18	Sequence 18, Appl
20	91	77.1	697	18	US-10-500-796A-11	Sequence 11, Appl
21	91	77.1	697	18	US-10-500-796A-18	Sequence 18, Appl
22	89	75.4	30	18	US-10-500-796A-34	Sequence 34, Appl
23	78	66.1	32	16	US-10-701-122-56	Sequence 56, Appl
24	75	63.6	24	18	US-10-500-796A-33	Sequence 33, Appl
25	56	47.5	108	16	US-10-437-963-195436	Sequence 195436, A
26	55	46.6	274	14	US-10-156-761-10960	Sequence 10960, A
27	51	43.2	79	9	US-09-738-626-4898	Sequence 4898, Ap
28	51	43.2	168	15	US-10-282-122A-51438	Sequence 51438, A
29	51	43.2	229	16	US-10-437-963-148577	Sequence 148577, A
30	51	43.2	412	9	US-09-738-626-5886	Sequence 5886, Ap
31	51	43.2	420	16	US-10-437-963-155427	Sequence 155427, A
32	50	42.4	166	18	US-10-450-763-48200	Sequence 48200, A
33	50	42.4	190	18	US-10-450-763-48198	Sequence 48198, A
34	50	42.4	328	9	US-09-738-626-3885	Sequence 3885, Ap
35	50	42.4	385	14	US-10-287-274-393	Sequence 393, App
36	50	42.4	426	18	US-10-450-763-48199	Sequence 48199, A
37	49.5	41.9	142	15	US-10-183-687-10	Sequence 10, Appl
38	49.5	41.9	424	15	US-10-183-687-497	Sequence 497, App
39	49.5	41.9	451	16	US-10-437-963-173411	Sequence 173411, A
40	49	41.5	120	9	US-09-764-847-714	Sequence 714, App
41	49	41.5	120	14	US-10-092-154-714	Sequence 714, App
42	49	41.5	204	15	US-10-634-548-29	Sequence 29, Appl
43	49	41.5	204	15	US-10-634-548-31	Sequence 31, Appl
44	49	41.5	328	18	US-10-830-828-26	Sequence 26, Appl
45	49	41.5	328	18	US-10-830-828-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1  
US-09-826-115-14  
; Sequence 14, Application US/09826115  
; Publication No. US20030022849A1  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Gwong-Jen J  
; TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of  
; FILE REFERENCE: 14114.0332U3  
; CURRENT APPLICATION NUMBER: US/09/826,115  
; CURRENT FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: pct/us99/12298  
; PRIOR FILING DATE: 1999-06-03  
; PRIOR APPLICATION NUMBER: 09/701,536  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/087,908  
; PRIOR FILING DATE: 1998-06-04  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 24  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence; note =  
; OTHER INFORMATION: synthetic construct  
; OTHER INFORMATION: JE Signal  
US-09-826-115-14

Query Match 100.0%; Score 118; DB 10; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2.5e-10;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGKRSAGSIMVLASLAVVIACAGA 24

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Db      1  MGKRSAGSIMWLASLAVVIACAGA 24
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence; note = synthetic construct
US-10-500-796A-37

RESULT 2
US-10-500-796A-14
; Sequence 14, Application US/10500796A
; Publication No. US20050163804A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services, Centers for Disease Control and Prevention
; APPLICANT: Chang, Gwong-Jen J.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION
; FILE REFERENCE: 6395-64909-02
; CURRENT APPLICATION NUMBER: US/10/500,796A
; PRIOR FILING DATE: 2004-07-06
; PRIOR APPLICATION NUMBER: PCT/US02/10764
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/826,115
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/12298
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 60/087,908
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence; note = synthetic construct
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: JE Signal
US-10-500-796A-14

Query Match      100.0%; Score 118; DB 18; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MGKRSAGSIMWLASLAVVIACAGA 24
|||||
Db      1  MGKRSAGSIMWLASLAVVIACAGA 24
|||||

RESULT 3
US-10-500-796A-37
; Sequence 37, Application US/10500796A
; Publication No. US20050163804A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services, Centers for Disease Control and Prevention
; APPLICANT: Chang, Gwong-Jen J.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION
; FILE REFERENCE: 6395-64909-02
; CURRENT APPLICATION NUMBER: US/10/500,796A
; PRIOR FILING DATE: 2004-07-06
; PRIOR APPLICATION NUMBER: PCT/US02/10764
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/826,115
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/12298
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 60/087,908
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 43
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-500-796A-43

Query Match      100.0%; Score 118; DB 18; Length 685;
Best Local Similarity 100.0%; Pred. No. 7e-09;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MGKRSAGSIMWLASLAVVIACAGA 24
|||||
Db      1  MGKRSAGSIMWLASLAVVIACAGA 24
|||||

RESULT 5
US-10-500-796A-45
; Sequence 45, Application US/10500796A
; Publication No. US20050163804A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services, Centers for Disease Control and Prevention
; APPLICANT: Chang, Gwong-Jen J.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION
; FILE REFERENCE: 6395-64909-02
; CURRENT APPLICATION NUMBER: US/10/500,796A
; CURRENT FILING DATE: 2004-07-06
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; PRIOR APPLICATION NUMBER: PCT/US02/10764  
; PRIOR FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: 09/826,115  
; PRIOR FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: 09/701,536  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/12298  
; PRIOR FILING DATE: 1999-06-03  
; PRIOR APPLICATION NUMBER: 60/087,908  
; PRIOR FILING DATE: 1998-06-04  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 45  
; LENGTH: 685  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-500-796A-45

Query Match 100.0%; Score 118; DB 18; Length 685;  
Best Local Similarity 100.0%; Pred. No. 7e-09; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGKRSAGSIMWLASLAVVIACAGA 24  
|||||  
DB 1 MGKRSAGSIMWLASLAVVIACAGA 24

RESULT 6  
US-10-500-796A-47  
; Sequence 47, Application US/10500796A  
; Publication No. US20050163804A1  
; GENERAL INFORMATION:  
; APPLICANT: The Government of the United States of America, as  
; APPLICANT: represented by the Secretary of the Department of Health and  
; APPLICANT: Human Services, Centers for Disease Control and Prevention  
; APPLICANT: Chang, Gwong-Jen J.  
; TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION  
; FILE REFERENCE: 6395-64909-02  
; CURRENT APPLICATION NUMBER: US/10/500,796A  
; CURRENT FILING DATE: 2004-07-06  
; PRIOR APPLICATION NUMBER: PCT/US02/10764  
; PRIOR FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: 09/826,115  
; PRIOR FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: 09/701,536  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/12298  
; PRIOR FILING DATE: 1999-06-03  
; PRIOR APPLICATION NUMBER: 60/087,908  
; PRIOR FILING DATE: 1998-06-04  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 47  
; LENGTH: 685  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-500-796A-47

Query Match 100.0%; Score 118; DB 18; Length 685;  
Best Local Similarity 100.0%; Pred. No. 7e-09; 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGKRSAGSIMWLASLAVVIACAGA 24  
|||||  
DB 1 MGKRSAGSIMWLASLAVVIACAGA 24

RESULT 7  
US-09-826-115-16

; Sequence 16, Application US/09826115  
; Publication No. US20030022849A1  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Gwong-Jen J.  
; TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of  
; TITLE OF INVENTION: Flavivirus Infection  
; FILE REFERENCE: 14114.0332U3  
; CURRENT APPLICATION NUMBER: US/09/826,115  
; CURRENT FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: PCT/US99/12298  
; PRIOR FILING DATE: 1999-06-03  
; PRIOR APPLICATION NUMBER: 09/701,536  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/087,908  
; PRIOR FILING DATE: 1998-06-04  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 692  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence; note =  
; OTHER INFORMATION: synthetic construct  
; OTHER INFORMATION: PCBWN  
US-09-826-115-16

Query Match 100.0%; Score 118; DB 10; Length 692;  
Best Local Similarity 100.0%; Pred. No. 7.1e-09;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGKRSAGSIMWLASLAVVIACAGA 24  
|||||  
DB 1 MGKRSAGSIMWLASLAVVIACAGA 24

RESULT 8  
US-10-500-796A-16  
; Sequence 16, Application US/10500796A  
; Publication No. US20050163804A1  
; GENERAL INFORMATION:  
; APPLICANT: The Government of the United States of America, as  
; APPLICANT: represented by the Secretary of the Department of Health and  
; APPLICANT: Human Services, Centers for Disease Control and Prevention  
; APPLICANT: Chang, Gwong-Jen J.  
; TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION  
; FILE REFERENCE: 6395-64909-02  
; CURRENT APPLICATION NUMBER: US/10/500,796A  
; CURRENT FILING DATE: 2004-07-06  
; PRIOR APPLICATION NUMBER: PCT/US02/10764  
; PRIOR FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: 09/826,115  
; PRIOR FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: 09/701,536  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/12298  
; PRIOR FILING DATE: 1999-06-03  
; PRIOR APPLICATION NUMBER: 60/087,908  
; PRIOR FILING DATE: 1998-06-04  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 16  
; LENGTH: 692  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-500-796A-16

Query Match 100.0%; Score 118; DB 18; Length 692;  
Best Local Similarity 100.0%; Pred. No. 7.1e-09;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MGKRSAGSIMWLASLAVVIACAGA 24
Db 1 MGKRSAGSIMWLASLAVVIACAGA 24

RESULT 9
US-09-826-115-27
; Sequence 27, Application US/09826115
; Publication No. US20030022849A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Gwong-Jen J
; TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of
; TITLE OF INVENTION: Flavivirus Infection
; FILE REFERENCE: 14114.033203
; CURRENT APPLICATION NUMBER: US/09/826,115
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: pct/us99/12298
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/087,908
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence; note =
; OTHER INFORMATION: synthetic construct
; OTHER INFORMATION: Modified JE Signal
US-09-826-115-27

Query Match 81.4%; Score 96; DB 10; Length 24;
Best Local Similarity 87.5%; Pred. No. 4.7e-07;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGKRSAGSIMWLASLAVVIACAGA 24
Db 1 MGKRSAGSIMWLASLAVVIAGTSA 24

RESULT 10
US-10-500-796A-27
; Sequence 27, Application US/10500796A
; Publication No. US20050163804A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services, Centers for Disease Control and Prevention
; APPLICANT: Chang, Gwong-Jen J.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION
; FILE REFERENCE: 6395-64909-02
; CURRENT APPLICATION NUMBER: US/10/500,796A
; CURRENT FILING DATE: 2004-07-06
; PRIOR APPLICATION NUMBER: PCT/US02/10764
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/826,115
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/12298
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 60/087,908
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence; note =
; OTHER INFORMATION: synthetic construct
; OTHER INFORMATION: Modified JE Signal
US-10-500-796A-27

Query Match 81.4%; Score 96; DB 10; Length 24;
Best Local Similarity 87.5%; Pred. No. 4.7e-07;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGKRSAGSIMWLASLAVVIACAGA 24
Db 1 MGKRSAGSIMWLASLAVVIAGTSA 24

RESULT 11
US-09-826-115-20
; Sequence 20, Application US/09826115
; Publication No. US20030022849A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Gwong-Jen J
; TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of
; TITLE OF INVENTION: Flavivirus Infection
; FILE REFERENCE: 14114.033203
; CURRENT APPLICATION NUMBER: US/09/826,115
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: pct/us99/12298
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/087,908
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence; note =
; OTHER INFORMATION: synthetic construct
; OTHER INFORMATION: Modified JE Signal
US-09-826-115-20

Query Match 81.4%; Score 96; DB 10; Length 681;
Best Local Similarity 87.5%; Pred. No. 1.3e-05;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGKRSAGSIMWLASLAVVIACAGA 24
Db 1 MGKRSAGSIMWLASLAVVIAGTSA 24

RESULT 12
US-09-826-115-24
; Sequence 24, Application US/09826115
; Publication No. US20030022849A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Gwong-Jen J
; TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of
; TITLE OF INVENTION: Flavivirus Infection
; FILE REFERENCE: 14114.033203
; CURRENT APPLICATION NUMBER: US/09/826,115
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: pct/us99/12298
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/087,908
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 681
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence; note =
; OTHER INFORMATION: synthetic construct
US-09-826-115-24

Query Match      81.4%; Score 96; DB 10; Length 681;
Best Local Similarity 87.5%; Pred. No. 1.3e-05;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MCKRSAGSIMMLASLAVVIACAGA 24
    |||||
DB 1 MCKRSAGSIMMLASLAVVIAGTSA 24
    |||||

RESULT 13
US-10-500-796A-24
; Sequence 24, Application US/10500796A
; Publication No. US20050163804A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services, Centers for Disease Control and Prevention
; APPLICANT: Chang, Gwong-Jen J.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION
; FILE REFERENCE: 6395-64909-02
; CURRENT APPLICATION NUMBER: US/10/500,796A
; CURRENT FILING DATE: 2004-07-06
; PRIOR APPLICATION NUMBER: PCT/US02/10764
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/826,115
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/12298
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 60/087,908
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-500-796A-24

Query Match      81.4%; Score 96; DB 18; Length 681;
Best Local Similarity 87.5%; Pred. No. 1.3e-05;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MCKRSAGSIMMLASLAVVIACAGA 24
    |||||
DB 1 MCKRSAGSIMMLASLAVVIAGTSA 24
    |||||

RESULT 14
US-10-500-796A-20
; Sequence 20, Application US/10500796A
; Publication No. US20050163804A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services, Centers for Disease Control and Prevention
; APPLICANT: Chang, Gwong-Jen J.
; TITLE OF INVENTION: NUCLEIC ACID VACCINES FOR PREVENTION OF FLAVIVIRUS INFECTION
; FILE REFERENCE: 6395-64909-02
; CURRENT APPLICATION NUMBER: US/10/500,796A
; CURRENT FILING DATE: 2004-07-06
; PRIOR APPLICATION NUMBER: PCT/US02/10764
; PRIOR FILING DATE: 2002-04-04
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; PRIOR APPLICATION NUMBER: 09/826,115
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/12298
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 60/087,908
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-500-796A-20

Query Match      81.4%; Score 96; DB 18; Length 685;
Best Local Similarity 87.5%; Pred. No. 1.3e-05;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MCKRSAGSIMMLASLAVVIACAGA 24
    |||||
DB 1 MCKRSAGSIMMLASLAVVIAGTSA 24
    |||||

RESULT 15
US-09-826-115-22
; Sequence 22, Application US/09826115
; Publication No. US20030022849A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Gwong-Jen J.
; TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of
; TITLE OF INVENTION: Flavivirus Infection
; FILE REFERENCE: 14114.033203
; CURRENT APPLICATION NUMBER: US/09/826,115
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/12298
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 09/701,536
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/087,908
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence; note =
; OTHER INFORMATION: synthetic construct
US-09-826-115-22

Query Match      81.4%; Score 96; DB 10; Length 692;
Best Local Similarity 87.5%; Pred. No. 1.3e-05;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MCKRSAGSIMMLASLAVVIACAGA 24
    |||||
DB 1 MCKRSAGSIMMLASLAVVIAGTSA 24
    |||||

Search completed: October 26, 2005, 01:48:45
Job time : 164 secs
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